

XX Alpha-conotoxin peptides that are used to treat disorders regulated
 PT at neuronal nicotinic acetylcholine receptors
 XX
 XX Claim 12; Page 27; 40pp; English.
 CC The present sequence represents a specifically claimed example of an
 CC alpha-conotoxin from the general formula given in AAY24155, which can be
 CC used to treat disorders regulated at neuronal nicotinic acetylcholine
 CC receptors (nAChR). The alpha-conotoxins are useful for preparing a
 CC pharmaceutical composition for treating disorders regulated at neuronal
 CC nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing
 CC disorders that can be treated include cardiovascular disorders, a
 CC gastric motility disorder, urinary incontinence, nicotine addiction, a
 CC mood disorder or small cell lung carcinoma. Mood disorders include
 CC bipolar disorder, unipolar depression, dysthymia and seasonal effective
 CC disorder. The alpha-conotoxins can also be used for diagnosis of small
 CC cell lung carcinoma. The alpha-conotoxin antagonists are able to
 CC discriminate between non-symmetrical ligand binding interfaces present
 CC on the nAChR. The alpha-conotoxin has the ability to potentially block any
 CC receptor containing an alpha beta subunit interface, regardless of what
 CC other subunits may be present in the receptor complex.
 CC
 XX Sequence 16 AA;
 SQ
 Query Match 100.0%; Score 104; DB 20; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCCSLPPCALNNDPYC 16
 Db 1 GCCSLPPCALNNDPYC 16
 RESULT 2
 AAY24163
 ID AAY24163 standard; peptide; 16 AA.
 XX
 AC AAY24163;
 XX
 DT 10-SEP-1999 (first entry)
 XX
 DE Alpha-conotoxin peptide SEQ ID NO:9.
 XX
 XX Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;
 KW small cell lung carcinoma; cardiovascular disorder; nicotine addiction;
 KW gastric motility disorder; urinary incontinence; mood disorder;
 KW bipolar disorder; unipolar depression; dysthymia;
 KW seasonal effective disorder.
 XX
 OS Conus purpurascens.
 XX
 PN WO9933482-A1.
 XX
 PD 08-JUL-1999.
 XX
 PF 23-DEC-1998; 98WO-US27367.
 XX
 PR 03-APR-1998; 98US-0080588.
 PR 31-DEC-1997; 97US-0070153.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Cartier GE, Luo S, McIntosh JM, Olivera BM, Yoshikami D;
 XX
 DR WPI: 1999-405367/34.
 XX
 PT Alpha-conotoxin peptides that are used to treat disorders regulated
 PT at neuronal nicotinic acetylcholine receptors
 XX
 PS Claim 28; Page 6; 40pp; English.
 CC The present sequence represents a specifically claimed example of an

CC alpha-conotoxin, which can be used to treat disorders regulated at
 CC neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins
 CC are useful for preparing a pharmaceutical composition for treating
 CC disorders regulated at neuronal nAChR, especially alpha 3 beta 2,
 CC alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be
 CC treated include cardiovascular disorders, a gastric motility disorder,
 CC urinary incontinence, nicotine addiction, a mood disorder or small cell
 CC lung carcinoma. Mood disorders include bipolar disorder, unipolar
 CC depression, dysthymia and seasonal effective disorder. The alpha-
 CC conotoxins can also be used for diagnosis of small cell lung carcinoma.
 CC The alpha-conotoxin antagonists are able to discriminate between non-
 CC symmetrical ligand binding interfaces present on the nAChR. The alpha-
 CC conotoxin has the ability to potentially block any receptor containing a
 CC alpha beta subunit interface, regardless of what other subunits may be
 CC present in the receptor complex.
 CC
 XX Sequence 16 AA;
 SQ
 Query Match 95.2%; Score 99; DB 20; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCCSLPPCALNNDPYC 16
 Db 1 GCCSLPPCALNNDPYC 16
 RESULT 3
 AAY24164
 ID AAY24164 standard; peptide; 16 AA.
 XX
 AC AAY24164;
 XX
 DT 10-SEP-1999 (first entry)
 XX
 DE Alpha-conotoxin peptide SEQ ID NO:12.
 XX
 XX Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;
 KW small cell lung carcinoma; cardiovascular disorder; nicotine addiction;
 KW gastric motility disorder; urinary incontinence; mood disorder;
 KW bipolar disorder; unipolar depression; dysthymia;
 KW seasonal effective disorder.
 XX
 OS Conus purpurascens.
 XX
 PN WO9933482-A1.
 XX
 PD 08-JUL-1999.
 XX
 PF 23-DEC-1998; 98WO-US27367.
 XX
 PR 03-APR-1998; 98US-0080588.
 PR 31-DEC-1997; 97US-0070153.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Cartier GE, Luo S, McIntosh JM, Olivera BM, Yoshikami D;
 XX
 DR WPI: 1999-405367/34.
 XX
 PT Alpha-conotoxin peptides that are used to treat disorders regulated
 PT at neuronal nicotinic acetylcholine receptors
 XX
 PS Claim 23; Page 6; 40pp; English.
 CC The present sequence represents a specifically claimed example of an
 CC alpha-conotoxin, which can be used to treat disorders regulated at
 CC neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins
 CC are useful for preparing a pharmaceutical composition for treating
 CC disorders regulated at neuronal nAChR, especially alpha 3 beta 2,
 CC alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be
 CC treated include cardiovascular disorders, a gastric motility disorder,
 CC urinary incontinence, nicotine addiction, a mood disorder or small cell

CC lung carcinoma. Mood disorders include bipolar disorder, unipolar
 CC depression, dysthymia and seasonal affective disorder. The alpha-
 CC conotoxin can also be used for diagnosis of small cell lung carcinoma.
 CC The alpha-conotoxin antagonists are able to discriminate between non-
 CC symmetrical ligand binding interfaces present on the nAChR. The alpha-
 CC conotoxin has the ability to potentially block any receptor containing a
 CC alpha beta subunit interface, regardless of what other subunits may be
 CC present in the receptor complex.

XX Sequence 16 AA:

Query Match 95.2%; Score 99; DB 20; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.3e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCSLPPCALNPDYC 16
 Db 1 GCCSLPPCALNPDYC 16

RESULT 4

AAM50844 standard; Peptide; 16 AA.

AC AAM50844;

DT 01-MAY-2002 (first entry)

DE Conus pennaceus Trk modulator peptide.

XX Trk: receptor tyrosine kinase; modulator; snail;

KW neurotrophic factor; NTF; mimetic; Huntington's disease;

KW Parkinson's disease; Alzheimer's disease;

KW amyotrophic lateral sclerosis; neurodegenerative disease; cancer;

KW neuroprotective; nootropic; anticonvulsant; antiparkinsonian;

KW cytoskeletal; therapy; cyclic.

OS Conus pennaceus.

XX WO200203071-A2.

XX 10-JAN-2002.

XX 05-JUL-2001; 2001WO-US21472.

XX 05-JUL-2000; 2000US-215778P.

XX (PANG-) PANGENE CORP.

XX Bates AT;

XX WPI: 2002-179638/23.

XX Screening for a neurotrophic factor mimetic, useful for treating, e.g.,

XX cancer and Alzheimer's, comprises combining a candidate mimetic with a

XX fragment of a tyrosine kinase protein

XX Claim 16; Page 10; 107pp; English.

XX The present sequence is that of a naturally-occurring cyclic

XX peptide from the tropical snail Conus pennaceus shell. The peptide

XX is capable of modulating the binding of a neurotrophin to a Trk

XX (receptor tyrosine kinase) protein, and of modulating the activity

XX of a Trk protein. The invention concerns Trks and their ligands

XX that modulate cell growth, differentiation and survival. Trk

XX proteins are known to mediate the activities of neurotrophins and

XX are also known proto-oncogenes. Methods are claimed for screening

XX for small molecule neurotrophic factor mimetics capable of

XX binding to a Trk protein or of modulating the binding of a

XX neurotrophin to a Trk protein. Also claimed are medicaments

XX comprising the present cyclic peptide for treatment of cancer or a

XX neurodegenerative disease selected from Huntington's disease,

XX Parkinson's disease, Alzheimer's disease and amyotrophic lateral

CC sclerosis.

XX Sequence 16 AA:

Query Match 95.2%; Score 99; DB 23; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.3e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCSLPPCALNPDYC 16
 Db 1 GCCSLPPCALNPDYC 16

RESULT 5

AAB21454 standard; Protein; 56 AA.

AC AAB21454;

DT 19-JAN-2001 (first entry)

DE Cone snail alpha-conotoxin SEQ ID NO: 115.

XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;

KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;

KW gastric motility disorder; urinary incontinence; nicotine addiction;

KW small cell lung carcinoma.

XX Conus pennaceus.

XX WO200044776-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US01979.

XX 29-JAN-1999; 99US-0118381.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX WPI: 2000-505965/45.

XX N-PADB; AAB94429.

XX alpha-conotoxin polypeptides derived from the venom of cone snails

XX useful e.g. as neuromuscular blocking agents for use in surgery and for

XX treating unipolar depression

XX Claim 39; Page 40; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and

XX their coding sequences from a number of different species of cone snail.

XX These peptides are found in minute quantities in the venom of the snails,

XX and are targeted at the neuronal nicotinic acetylcholine receptors of the

XX nervous system. They usually contain two disulphide bonds, which give

XX them defined conformations, a rarity in molecules this small. The

XX alpha-conotoxins can be used as neuromuscular blocking agents in surgery,

XX and for treating disorders regulated at the neuronal nicotinic

XX acetylcholine receptors, including cardiovascular disorders, gastric

XX motility disorders, urinary incontinence, nicotine addiction, mood

XX disorders such as bipolar disorder, unipolar depression, dysthymia and

XX seasonal affective disorder, and small cell lung carcinoma.

XX Sequence 56 AA;

Query Match 91.3%; Score 95; DB 21; Length 56;
 Best Local Similarity 87.5%; Pred. No. 0.00011;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCSLPPCALNPDYC 16
 Db 1 GCCSLPPCALNPDYC 16

Db 40 GCCSHPPCANNDPYC 55

RESULT 6

AAV24159 standard; peptide; 16 AA.

AAV24159;

10-SEP-1999 (first entry)

Alpha-conotoxin peptide SEQ ID NO:11.

Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;
small cell lung carcinoma; cardiovascular disorder; nicotine addiction;
gastric motility disorder; urinary incontinence; mood disorder;
bipolar disorder; unipolar depression; dysthymia;
seasonal affective disorder.

Conus sp.
Synthetic.

WO933482-A1.

08-JUL-1999.

23-DEC-1998; 98WO-US27367.

03-APR-1998; 98US-0080588.

31-DEC-1997; 97US-0070153.

(UTAH) UNIV UTAH RES FOUND.

Cartier GE, Luo S, McIntosh JM, Olivera BM, Yoshikami D;

WPI; 1999-405367/34.

Alpha-conotoxin peptides that are used to treat disorders regulated
at neuronal nicotinic acetylcholine receptors

Claim 12; Page 27; 40pp; English.

The present sequence represents a specifically claimed example of an
alpha-conotoxin from the general formula given in AAV24159, which can be
used to treat disorders regulated at neuronal nicotinic acetylcholine
receptors (nAChR). The alpha-conotoxins are useful for preparing a
pharmaceutical composition for treating disorders regulated at neuronal
nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing
nAChR. Disorders that can be treated include cardiovascular disorders, a
gastric motility disorder, urinary incontinence, nicotine addiction, a
mood disorder or small cell lung carcinoma. Mood disorders include
bipolar disorder, unipolar depression, dysthymia and seasonal affective
disorder. The alpha-conotoxins can also be used for diagnosis of small
cell lung carcinoma. The alpha-conotoxin antagonists are able to
discriminate between non-symmetrical ligand binding interfaces present
on the nAChR. The alpha-conotoxin has the ability to potentially block any
receptor containing an alpha beta subunit interface, regardless of what
other subunits may be present in the receptor complex.

Sequence 16 AA;

Query Match 90.4%; Score 94; DB 20; Length 16;

Best Local Similarity 87.5%; Pred. No. 5.2e-05;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 GCCSLPPCALNNDPYC 16

1 GCCSLPPCAASNDPYC 16

RESULT 7
AAB21455
ID AAB21455 standard; Protein; 56 AA.

XX AAB21455;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 117.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;
small cell lung carcinoma.

Conus pennaceus.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US01979.

29-JAN-1999; 99US-0118381.

(UTAH) UNIV UTAH RES FOUND.
(COGN-) COGNEX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.

N-PSDB; AAA89430.

alpha-conotoxin polypeptides derived from the venom of cone snails
useful e.g. as neuromuscular blocking agents for use in surgery and for
treating unipolar depression -

Claim 39; Page 40; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and
their coding sequences from a number of different species of cone snail.
These peptides are found in minute quantities in the venom of the snails,
and are targeted at the neuronal nicotinic acetylcholine receptors of the
nervous system. They usually contain two disulphide bonds, which give
them defined conformations, a rarity in molecules this small. The
alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
and for treating disorders regulated at the neuronal nicotinic
acetylcholine receptors, including cardiovascular disorders, gastric
motility disorders, urinary incontinence, nicotine addiction, mood
disorders such as bipolar disorder, unipolar depression, dysthymia and
seasonal affective disorder, and small cell lung carcinoma.

Sequence 56 AA;

Query Match 87.5%; Score 91; DB 21; Length 56;

Best Local Similarity 87.5%; Pred. No. 0.00035;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 GCCSLPPCALNNDPYC 16

40 GCCSHPPCALNNDPYC 55

RESULT 8

AAB21615

19-JAN-2001 (first entry)

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 358.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;

KW small cell lung carcinoma.
 XX
 OS Conus obscurus.
 XX
 PN W0200044776-A1.
 XX
 PD 03-AUG-2000.
 XX
 PE 28-JAN-2000; 2000WO-US01979.
 XX
 PR 29-JAN-1999; 99US-0118381.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX
 PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;
 XX
 DR WPI; 2000-505965/45.
 DR N-PSDB; AAA89511.
 XX
 PT alpha-conotoxin polypeptides derived from the venom of cone snails
 PT useful e.g. as neuromuscular blocking agents for use in surgery and for
 PT treating unipolar depression -
 XX
 PS Claim 39; Page 61; 229pp; English.
 XX
 CC The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The
 CC alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
 CC and for treating disorders regulated at the neuronal nicotinic
 CC acetylcholine receptors, including cardiovascular disorders, gastric
 CC motility disorders, urinary incontinence, nicotine addiction, mood
 CC disorders such as bipolar disorder, unipolar depression, dysthymia and
 CC seasonal affective disorder, and small cell lung carcinoma.
 CC
 XX
 SQ Sequence 56 AA;
 Query Match 79.8%; Score 83; DB 21; Length 56;
 Best Local Similarity 81.2%; Pred. No. 0.0032;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GCCSPPCALNNPDYC 16
 |||||
 DT 19-JAN-2001 (first entry)
 XX
 DE Cone snail alpha-conotoxin SEQ ID NO: 67.
 XX
 KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.
 XX
 OS Conus textile.
 XX
 PN W0200044776-A1.
 XX
 PD 03-AUG-2000.
 XX
 PE 28-JAN-2000; 2000WO-US01979.
 XX

PR 29-JAN-1999; 99US-0118381.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX
 PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;
 XX
 DR WPI; 2000-505965/45.
 DR N-PSDB; AAA89405.
 XX
 PT alpha-conotoxin polypeptides derived from the venom of cone snails
 PT useful e.g. as neuromuscular blocking agents for use in surgery and for
 PT treating unipolar depression -
 XX
 PS Claim 39; Page 33; 229pp; English.
 XX
 CC The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The
 CC alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
 CC and for treating disorders regulated at the neuronal nicotinic
 CC acetylcholine receptors, including cardiovascular disorders, gastric
 CC motility disorders, urinary incontinence, nicotine addiction, mood
 CC disorders such as bipolar disorder, unipolar depression, dysthymia and
 CC seasonal affective disorder, and small cell lung carcinoma.
 CC
 XX
 SQ Sequence 56 AA;
 Query Match 76.9%; Score 80; DB 21; Length 56;
 Best Local Similarity 75.0%; Pred. No. 0.0074;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GCCSPPCALNNPDYC 16
 |||||
 DT 19-JAN-2001 (first entry)
 XX
 DE Cone snail alpha-conotoxin SEQ ID NO: 133.
 XX
 KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.
 XX
 OS Conus dalli.
 XX
 PN W0200044776-A1.
 XX
 PD 03-AUG-2000.
 XX
 PE 28-JAN-2000; 2000WO-US01979.
 XX
 PR 29-JAN-1999; 99US-0118381.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX
 PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;
 XX
 DR WPI; 2000-505965/45.
 DR N-PSDB; AAA89438.
 XX

PT alpha-conotoxin polypeptides derived from the venom of cone snails
 PT useful e.g. as neuromuscular blocking agents for use in surgery and for
 PT treating unipolar depression -
 XX
 PS Claim 39; Page 42-43; 229pp; English.

CC The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The
 CC alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
 CC and for treating disorders regulated at the neuronal nicotinic
 CC acetylcholine receptors, including cardiovascular disorders, gastric
 CC motility disorders, urinary incontinence, nicotine addiction, mood
 CC disorders such as bipolar disorder, unipolar depression, dysthymia and
 CC seasonal affective disorder, and small cell lung carcinoma.

Sequence 59 AA;

Query Match 76.9%; Score 80; DB 21; Length 59;
 Best Local Similarity 75.0%; Pred. No. 0.0078;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDYC 16
 DB 40 GCCSRPCIANNPDLG 55

RESULT 11

AAB21620
 ID AAB21620 standard; Peptide; 21 AA.

AC AAB21620;

DT 19-JAN-2001 (first entry)

DE Cone snail alpha-conotoxin SEQ ID NO: 368.

XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.

OS Conus omaria.

PN WO200044776-A1.

PD 03-AUG-2000.

PF 28-JAN-2000; 2000WO-US01979.

PR 29-JAN-1999; 99US-0118381.

PA (UTAH) UNIV UTAH RES FOUNDD.

PA (COGN-) COGNETIX INC.

PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

DR WPI: 2000-505965/45.

DR N-PSDB; AAA89516.

PT alpha-conotoxin polypeptides derived from the venom of cone snails
 PT useful e.g. as neuromuscular blocking agents for use in surgery and for
 PT treating unipolar depression -
 XX

PS Claim 39; Page 62; 229pp; English.

CC The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the

CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The
 CC alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
 CC and for treating disorders regulated at the neuronal nicotinic
 CC acetylcholine receptors, including cardiovascular disorders, gastric
 CC motility disorders, urinary incontinence, nicotine addiction, mood
 CC disorders such as bipolar disorder, unipolar depression, dysthymia and
 CC seasonal affective disorder, and small cell lung carcinoma.

Sequence 21 AA;

Query Match 76.0%; Score 79; DB 21; Length 21;
 Best Local Similarity 75.0%; Pred. No. 0.0043;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDYC 16
 DB 5 GCCSDPSCNVNPDYC 20

RESULT 12

AAB21459
 ID AAB21459 standard; Protein; 56 AA.

AC AAB21459;

DT 19-JAN-2001 (first entry)

DE Cone snail alpha-conotoxin SEQ ID NO: 125.

XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.

OS Conus episcopatus.

PN WO200044776-A1.

PD 03-AUG-2000.

PF 28-JAN-2000; 2000WO-US01979.

PR 29-JAN-1999; 99US-0118381.

PA (UTAH) UNIV UTAH RES FOUNDD.

PA (COGN-) COGNETIX INC.

PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

DR WPI: 2000-505965/45.

DR N-PSDB; AAA89434.

PT alpha-conotoxin polypeptides derived from the venom of cone snails
 PT useful e.g. as neuromuscular blocking agents for use in surgery and for
 PT treating unipolar depression -
 XX

PS Claim 39; Page 41; 229pp; English.

CC The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The
 CC alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
 CC and for treating disorders regulated at the neuronal nicotinic
 CC acetylcholine receptors, including cardiovascular disorders, gastric
 CC motility disorders, urinary incontinence, nicotine addiction, mood
 CC disorders such as bipolar disorder, unipolar depression, dysthymia and
 CC seasonal affective disorder, and small cell lung carcinoma.

Sequence 56 AA;

Query Match 76.0%; Score 79; DB 21; Length 56;
Best Local Similarity 75.0%; Pred. No. 0.0098;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNNDPDC 16
|||||:|||||
DB 40 GCCSDPRCMMNNDPDC 55

RESULT 13
AAR75274
ID AAR75274 standard; peptide: 16 AA.

XX AAR75274;
XX 21-DEC-1995 (first entry)
XX A-1 lineage conotoxin BN-1 peptide.

XX Conotoxin; neuromuscular; synapse; signal transmission; inhibitor.
XX Conus bandanans.

XX Key location/Qualifiers
FT Misc-difference 6 /label- Pro or OTHER
FT Misc-difference 13 /note= "Hydroxyproline"
FT Misc-difference 13 /label- Pro or OTHER
FT Modified-site 14 /note= "Hydroxyproline"

FT Modified-site 16 /note= "Asp, can form a peptide bond via either
FT Modified-site 16 /note= "Hydroxyproline"
FT Modified-site 16 /note= "preferably amidated"

XX W09511256-A1.
XX 27-APR-1995.
XX 19-OCT-1994; 94WO-US11927.
XX 19-OCT-1993; 93US-0137800.

XX (UTAH) UNIV UTAH RES FOUND.
XX Cruz LJ, Hillyard DR, McIntosh JM, Olivera BM, Santos AD;
XX WPI: 1995-170189/22.
XX New A-1 lineage conotoxin peptide(s) - which inhibit synaptic
XX transmission at the neuromuscular junction or are active against
XX potassium or sodium channels

XX Claim 1: Page 41; 66pp; English.
XX The kappa-conotoxin, alpha conotoxin and alpha-1 like conotoxin
XX peptides all belong to a group of peptides known as the A-1 lineage
XX conotoxin peptides. The A-1 lineage conotoxin peptides have a wide
XX variety of pharmacological uses. The A-1 lineage conotoxin peptides
XX claimed (AAR75264-R75293) are useful for the inhibition of synaptic
XX transmission at neuromuscular junctions by blocking nicotinic acetyl
XX choline receptors and they also have activity against voltage-gated Na
XX and K channels.

XX Sequence 16 AA;

Query Match 72.1%; Score 75; DB 16; Length 16;
Best Local Similarity 68.8%; Pred. No. 0.01;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNNDPDC 16

DB 1 GCCSHPACSVNNDPDC 16
|||||:|||||

RESULT 14
AAB21609
ID AAB21609 standard; Peptide: 38 AA.
XX AAB21609;
XX 19-JAN-2001 (first entry)

XX Cone snail alpha-conotoxin SEQ ID NO: 346.
XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
XX neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
XX gastric motility disorder; urinary incontinence; nicotine addiction;
XX small cell lung carcinoma.

XX Conus marmoreus.
XX W0200044776-A1.
XX 03-AUG-2000.
XX 28-JAN-2000; 2000WO-US01979.

XX 29-JAN-1999; 99US-0118381.
XX (UTAH) UNIV UTAH RES FOUND.
XX (COGN-) COGNETIX INC.
XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;
XX WPI: 2000-505965/45.
XX N-PSDB; AAB89505.

XX alpha-conotoxin polypeptides derived from the venom of cone snails
XX useful e.g. as neuromuscular blocking agents for use in surgery and for
XX treating unipolar depression .
XX Claim 39; Page 59; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and
XX their coding sequences from a number of different species of cone snail.
XX These peptides are found in minute quantities in the venom of the snails,
XX and are targeted at the neuronal nicotinic acetylcholine receptors of the
XX nervous system. They usually contain two disulphide bonds, which give
XX them defined conformations, a rarity in molecules this small. The
XX alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
XX and for treating disorders regulated at the neuronal nicotinic
XX acetylcholine receptors, including cardiovascular disorders, gastric
XX motility disorders, urinary incontinence, nicotine addiction, mood
XX disorders such as bipolar disorder, unipolar depression, dysthymia and
XX seasonal affective disorder, and small cell lung carcinoma.

XX Sequence 38 AA;
XX Query Match 72.1%; Score 75; DB 21; Length 38;
XX Best Local Similarity 68.8%; Pred. No. 0.021;
XX Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNNDPDC 16
|||||:|||||

DB 22 GCCSHPACSVNNDPDC 37

RESULT 15
AAB21435
ID AAB21435 standard; Protein: 60 AA.
XX AAB21435;
XX

DT 19-JAN-2001 (first entry)
 XX
 DE Cone snail alpha-conotoxin SEQ ID NO: 77.
 XX
 KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.
 XX
 OS Conus bandanus.
 XX
 PN WO200044776-A1.
 PD 03-AUG-2000.
 XX
 PF 28-JAN-2000; 2000WO-US01979.
 XX
 PR 29-JAN-1999; 99US-0118381.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX
 PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM.
 XX
 DR WPI; 2000-505965/45.
 DR N-PDB; AAA89410.
 XX
 PT alpha-conotoxin polypeptides derived from the venom of cone snails
 PT useful e.g. as neuromuscular blocking agents for use in surgery and for
 PT treating unipolar depression -
 XX
 PS Claim 39; Page 34; 229pp; English.
 XX
 CC The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The
 CC alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
 CC and for treating disorders regulated at the neuronal nicotinic
 CC acetylcholine receptors, including cardiovascular disorders, gastric
 CC motility disorders, urinary incontinence, nicotine addiction, mood
 CC disorders such as bipolar disorder, unipolar depression, dysthymia and
 CC seasonal affective disorder, and small cell lung carcinoma.
 XX
 SQ Sequence 60 AA;

 Query Match 72.1%; Score 75; DB 21; Length 60;
 Best Local Similarity 68.8%; Pred. No. 0.032;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

 QY 1 GCCSLPPCALNNDYC 16
 ||||| |::|||
 DB 44 GCCSHRACSYNNPDIC 59

Search completed: January 8, 2003, 15:28:35
 Job time : 31.0606 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 8, 2003, 15:27:29 : Search time 11.1515 Seconds
(without alignments)
42.215 Million cell updates/sec

Title: US-09-897-465-10
Perfect score: 104
Sequence: 1 GCCSLPPCALNPDYC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	16	4	US-09-219-446B-10
2	99	95.2	16	4	US-09-219-446B-9
3	99	95.2	16	4	US-09-219-446B-12
4	94	90.4	16	4	US-09-219-446B-11
5	75	72.1	65	1	US-08-137-800-46
6	75	72.1	65	1	US-08-477-383-46
7	75	72.1	65	1	US-08-487-174-46
8	75	72.1	65	1	US-08-480-750-46
9	74	71.2	16	2	US-08-857-068-2
10	74	71.2	16	4	US-09-219-446B-5
11	74	71.2	17	4	US-09-219-446B-6
12	67	64.4	16	2	US-08-857-068-4
13	67	64.4	16	4	US-09-219-446B-8
14	66	63.5	15	2	US-08-857-068-3
15	65	62.5	65	4	US-09-488-799-95
16	64	61.5	63	4	US-09-488-799-93
17	64	61.5	63	4	US-09-488-799-99
18	60	57.7	18	1	US-08-137-800-32
19	60	57.7	18	1	US-08-477-383-32
20	60	57.7	18	1	US-08-487-174-32
21	60	57.7	18	1	US-08-480-750-32
22	60	57.7	62	4	US-09-488-799-89
23	59	56.7	63	4	US-09-488-799-97
24	58	55.8	15	4	US-09-219-446B-7
25	56	53.8	44	4	US-09-488-799-91
26	56	53.8	62	4	US-09-488-799-101
27	55	52.9	20	1	US-08-137-800-18

28	55	52.9	20	1	US-08-477-383-18	Sequence 18, App1
29	55	52.9	20	1	US-08-487-174-18	Sequence 18, App1
30	55	52.9	20	1	US-08-480-750-18	Sequence 18, App1
31	55	52.9	68	1	US-08-137-800-47	Sequence 47, App1
32	55	52.9	68	1	US-08-477-383-47	Sequence 47, App1
33	55	52.9	68	1	US-08-487-174-47	Sequence 47, App1
34	55	52.9	68	1	US-08-480-750-47	Sequence 47, App1
35	55	52.9	70	1	US-08-137-800-49	Sequence 49, App1
36	55	52.9	70	1	US-08-477-383-49	Sequence 49, App1
37	55	52.9	70	1	US-08-487-174-49	Sequence 49, App1
38	55	52.9	70	1	US-08-480-750-49	Sequence 49, App1
39	50	48.1	16	1	US-08-137-800-14	Sequence 14, App1
40	50	48.1	16	1	US-08-477-383-14	Sequence 14, App1
41	50	48.1	16	1	US-08-477-383-54	Sequence 54, App1
42	50	48.1	16	1	US-08-487-174-54	Sequence 54, App1
43	50	48.1	16	1	US-08-480-750-54	Sequence 54, App1
44	50	48.1	16	1	US-08-480-750-14	Sequence 14, App1
45	50	48.1	16	1	US-08-480-750-54	Sequence 54, App1

ALIGNMENTS

RESULT 1
US-09-219-446B-10
Sequence 10, Application US/09219446B
Patent No. 6265541

GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Siglin
TITLE OF INVENTION: Uses of Utah Research Foundation
FILE REFERENCE: Uses of Alpha-Conotoxin Peptides
CURRENT APPLICATION NUMBER: US/09/219,446B
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: A10L derivative
US-09-219-446B-10

Query Match 100.0%; Score 104; DB 4; Length 16;
Best local similarity 100.0%; Pred. No. 9.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDYC 16
DB 1 GCCSLPPCALNPDYC 16

RESULT 2
US-09-219-446B-9
Sequence 9, Application US/09219446B
Patent No. 6265541
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Siglin
APPLICANT: University of Utah Research Foundation

;; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
;; FILE REFERENCE: Uses of Alpha-Conotoxins
;; CURRENT APPLICATION NUMBER: US/09/219,446B
;; CURRENT FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: US 60/080,588
;; PRIOR FILING DATE: 1998-04-03
;; PRIOR APPLICATION NUMBER: US 60/070,153
;; PRIOR FILING DATE: 1997-12-31
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 9
;; LENGTH: 16
;; TYPE: PRT
;; ORGANISM: Conus purpurascens
US-09-219-446B-9

Query Match 95.2%; Score 99; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNNDYC 16
Db 1 GCCSLPPCALNNDYC 16

RESULT 3
US-09-219-446B-12
;; Sequence 12, Application US/09219446B
;; Patent No. 6265541
;; GENERAL INFORMATION:
;; APPLICANT: Olivera, Baldomero M.
;; APPLICANT: McIntosh, J. Michael
;; APPLICANT: Yoshikami, Doju
;; APPLICANT: Cartier, G. Edward
;; APPLICANT: Luo, Siglin
;; APPLICANT: University of Utah Research Foundation
;; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
;; FILE REFERENCE: Uses of Alpha-Conotoxins
;; CURRENT APPLICATION NUMBER: US/09/219,446B
;; CURRENT FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: US 60/080,588
;; PRIOR FILING DATE: 1998-04-03
;; PRIOR APPLICATION NUMBER: US 60/070,153
;; PRIOR FILING DATE: 1997-12-31
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 12
;; LENGTH: 16
;; TYPE: PRT
;; ORGANISM: Conus purpurascens
US-09-219-446B-12

Query Match 95.2%; Score 99; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNNDYC 16
Db 1 GCCSLPPCALNNDYC 16

RESULT 4
US-09-219-446B-11
;; Sequence 11, Application US/09219446B
;; Patent No. 6265541
;; GENERAL INFORMATION:
;; APPLICANT: Olivera, Baldomero M.
;; APPLICANT: McIntosh, J. Michael
;; APPLICANT: Yoshikami, Doju
;; APPLICANT: Cartier, G. Edward
;; APPLICANT: Luo, Siglin
;; APPLICANT: University of Utah Research Foundation
;; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

;; FILE REFERENCE: Uses of Alpha-Conotoxins
;; CURRENT APPLICATION NUMBER: US/09/219,446B
;; CURRENT FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: US 60/080,588
;; PRIOR FILING DATE: 1998-04-03
;; PRIOR APPLICATION NUMBER: US 60/070,153
;; PRIOR FILING DATE: 1997-12-31
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 11
;; LENGTH: 16
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: N1LS derivative
US-09-219-446B-11

Query Match 90.4%; Score 94; DB 4; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNNDYC 16
Db 1 GCCSLPPCALNNDYC 16

RESULT 5
US-08-137-800-46
;; Sequence 46, Application US/08137800
;; Patent No. 5514774
;; GENERAL INFORMATION:
;; APPLICANT: Olivera, Baldomero M.
;; APPLICANT: Cruz, Lourdes J.
;; APPLICANT: Hilliard, David R.
;; APPLICANT: McIntosh, J. Michael
;; APPLICANT: Santos, Aurefina D.
;; TITLE OF INVENTION: Conotoxin Peptides
;; NUMBER OF SEQUENCES: 53
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
;; STREET: 1201 New York Avenue N.W., Suite 1000
;; CITY: Washington
;; STATE: DC
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Wordperfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/137,800
;; FILING DATE: 19-OCT-1993
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ihnen, Jeffrey L.
;; REGISTRATION NUMBER: 28,957
;; REFERENCE/DOCKET NUMBER: 24260-104763
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-962-4810
;; TELEFAX: 202-962-8300
;; INFORMATION FOR SEQ ID NO: 46:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 65 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Conus bandanus
US-08-137-800-46

Query Match 72.1%; Score 75; DB 1; Length 65;
Best Local Similarity 68.8%; Pred. No. 0.0096;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDYC 16
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Db 49 GCCSHFACSVNPDIC 64

RESULT 6
US-08-477-383-46
; Sequence 46, Application US/08477383
; Patent No. 5589340
; GENERAL INFORMATION:
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,383
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus bandanus
; US-08-477-383-46

Query Match 72.1%; Score 75; DB 1; Length 65;
Best Local Similarity 68.8%; Pred. No. 0.0096;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDYC 16
|||||:::|||||
Db 49 GCCSHFACSVNPDIC 64

RESULT 7
US-08-487-174-46

; Sequence 46, Application US/08487174
; Patent No. 5595972
; GENERAL INFORMATION:
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,174
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus bandanus
; US-08-487-174-46

Query Match 72.1%; Score 75; DB 1; Length 65;
Best Local Similarity 68.8%; Pred. No. 0.0096;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDYC 16
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Db 49 GCCSHFACSVNPDIC 64

RESULT 8
US-08-480-750-46
; Sequence 46, Application US/08480750
; Patent No. 563347
; GENERAL INFORMATION:
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus bandanus
US-08-480-750-46
Query Match 72.1%; Score 75; DB 1; Length 65;
Best Local Similarity 68.8%; Pred. No. 0.0096;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCCSLPPCALNPDYC 16
DB 49 GCCSHRACSVNPDIC 64
RESULT 9
US-08-857-068-2
Sequence 2, Application US/08857068
Patent No. 5866682
GENERAL INFORMATION:
APPLICANT: McIntosh, J. Michael
APPLICANT: Cartier, G. Edward
APPLICANT: Yoshikami, Doju
APPLICANT: Luo, Siglin
APPLICANT: Oliveira, Baldomero M.
TITLE OF INVENTION: CONOPEPTIDES AURA, AURA AND AURA
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,068
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-121388
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Conus aulicus
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 2..8
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 3..16
US-08-857-068-2

Query Match 71.2%; Score 74; DB 2; Length 16;
Best Local Similarity 68.8%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDYC 16
DB 1 GCCSYPCFATNSDYC 16

RESULT 10
US-09-219-446B-5
Sequence 5, Application US/09219446B
Patent No. 6265541
GENERAL INFORMATION:
APPLICANT: Oliveira, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Siglin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/219,446B
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 16
TYPE: PRT
ORGANISM: Conus aulicus
US-09-219-446B-5

Query Match 71.2%; Score 74; DB 4; Length 16;
Best Local Similarity 68.8%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GCCSLPPCALNPDYC 16
DB 1 GCCSYPCFATNSDYC 16


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RESULT 11
US-09-219-446B-6
; Sequence 6, Application US/09219446B
; Patent No. 6265541
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/219,446B
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tyr derivative
US-09-219-446B-6

Query Match          71.2%; Score 74; DB 4; Length 17;
Best Local Similarity 68.8%; Pred. No. 0.0037;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GCCSLPPCALNPDYC 16
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Db      2 GCCSYPCFATNSDYC 17

RESULT 12
US-08-857-068-4
; Sequence 4, Application US/08857068
; Patent No. 5866682
; GENERAL INFORMATION:
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Cartier, G. Edward
; APPLICANT: Yoshikami, Doju
; APPLICANT: Luo, Siglin
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: CONOPEPTIDES AULA, AUIB AND AUIC
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/857,068
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-121388
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810

```

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; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Conus aulicus
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 2..8
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 3..16
US-08-857-068-4

Query Match          64.4%; Score 67; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 GCCSLPPCALNPDYC 16
      ||| ||| | |||
Db      1 GCCSYPCFATNSGYC 16

RESULT 13
US-09-219-446B-8
; Sequence 8, Application US/09219446B
; Patent No. 6265541
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/219,446B
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus aulicus
US-09-219-446B-8

Query Match          64.4%; Score 67; DB 4; Length 16;
Best Local Similarity 62.5%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 GCCSLPPCALNPDYC 16
      ||| ||| | |||
Db      1 GCCSYPCFATNSGYC 16

RESULT 14
US-08-857-068-3
; Sequence 3, Application US/08857068
; Patent No. 5866682
; GENERAL INFORMATION:
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Cartier, G. Edward
; APPLICANT: Yoshikami, Doju
; APPLICANT: Luo, Siglin
; APPLICANT: Olivera, Baldomero M.

```

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; TITLE OF INVENTION: CONOPEPTIDES AUA, AUB AND AUC
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/857,068
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-121388
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Conus aulicus
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 2..8
; NAME/KEY: Disulfide-bond
; LOCATION: 3..15
; US-08-857-068-3

Query Match      63.5%; Score 66; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPD 14
Db 1 GCCSYPPCWFATPD 14

RESULT 15
US-09-488-799-95
; Sequence 95, Application US/09488799
; Patent No. 6268473
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Layer, Richard T.
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Schoenfeld, Robert
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Alpha Conotoxin Peptides
; FILE REFERENCE: Alphas 1
; CURRENT APPLICATION NUMBER: US/09/488,799
; EARLIER FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: 60/116,881
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/116,882
; EARLIER FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 95
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Conus sulcatus
; US-09-488-799-95

Query Match      62.5%; Score 65; DB 4; Length 65;
Best Local Similarity 56.2%; Pred. No. 0.15;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDYC 16
Db 46 GCCSYPPCWFVSYPEIC 61

Search completed: January 8, 2003, 15:30:57
Job time : 12.1515 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 15:30:00 ; Search time 7.27273 Seconds
(without alignments)
42.682 Million cell updates/sec

Title: US-09-897-465-10
Perfect score: 104
Sequence: 1 GCCSLPPCALNPDYC 16

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Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	99	95.2	16	10	US-09-897-465-9
3	99	95.2	16	10	US-09-897-465-12
4	94	90.4	16	10	US-09-897-465-11
5	74	71.2	16	10	US-09-897-465-5
6	74	71.2	16	10	US-09-897-465-6
7	67	64.4	16	10	US-09-897-465-8
8	58	55.8	16	10	US-09-897-465-7
9	50	48.1	16	10	US-09-897-465-2
10	50	48.1	17	10	US-09-897-465-3
11	47	45.2	52	10	US-09-864-761-47370
12	47	45.2	218	12	US-10-116-064-3
13	45	43.3	16	10	US-09-897-465-4
14	43	41.3	34	10	US-09-864-761-40671
15	42.5	40.9	97	10	US-09-867-550-1022
16	42.5	40.9	469	10	US-09-925-301-1377
17	42.5	40.9	1924	9	US-09-866-5574-2
18	42.5	40.9	4545	10	US-09-873-403-2
19	42	40.4	12	10	US-09-897-465-13

20	41	39.4	101	10	US-09-764-877-1470	Sequence 1470, Ap
21	41	39.4	113	10	US-09-925-300-1460	Sequence 1460, Ap
22	41	39.4	102	10	US-09-727-238-4	Sequence 4, Appl1
23	40.5	38.9	438	9	US-09-997-598-129	Sequence 129, Ap
24	40.5	38.9	438	9	US-09-988-293A-129	Sequence 129, Ap
25	40.5	38.9	438	9	US-09-989-735-129	Sequence 129, Ap
26	40.5	38.9	438	9	US-09-990-444-129	Sequence 129, Ap
27	40.5	38.9	438	9	US-09-989-730-129	Sequence 129, Ap
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31	40.5	38.9	438	9	US-09-989-734-129	Sequence 129, Ap
32	40.5	38.9	438	10	US-09-989-722-129	Sequence 129, Ap
33	40.5	38.9	438	10	US-09-989-723-129	Sequence 129, Ap
34	40.5	38.9	438	10	US-09-989-279-129	Sequence 129, Ap
35	40.5	38.9	438	10	US-09-989-727-129	Sequence 129, Ap
36	40.5	38.9	438	10	US-09-989-731-129	Sequence 129, Ap
37	40.5	38.9	438	10	US-09-989-732-129	Sequence 129, Ap
38	40.5	38.9	438	10	US-09-991-073-129	Sequence 129, Ap
39	40.5	38.9	438	10	US-09-990-442-129	Sequence 129, Ap
40	40.5	38.9	438	10	US-09-991-163-129	Sequence 129, Ap
41	40.5	38.9	438	10	US-09-993-604-129	Sequence 129, Ap
42	40.5	38.9	438	10	US-09-990-456-129	Sequence 129, Ap
43	40.5	38.9	438	10	US-09-989-721-129	Sequence 129, Ap
44	40.5	38.9	438	12	US-10-052-586-110	Sequence 110, Ap
45	40.5	38.9	474	10	US-09-808-387-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-09-897-465-10
Sequence 10, Application US/09897465
Patent No. US2002022715A1
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Carter, G. Edward
APPLICANT: Luo, Siqin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxins
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/897,465
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: A10L derivative
US-09-897-465-10
Query Match 100.0%; Score 104; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCSLPPCALNPDYC 16
DB 1 GCCSLPPCALNPDYC 16
RESULT 2
US-09-897-465-9
Sequence 9, Application US/09897465

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; Patent No. US20020022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxins
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-09-897-465-9
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Query Match          95.2%; Score 99; DB 10; Length 16;
Best Local Similarity 93.8%; Pred. No. 4.3e-07;
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OY 1 GCCSLPPCALNNDPDC 16
DB 1 GCCSLPPCALNNDPDC 16
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RESULT 3
; Sequence 12, Application US/09897465
; Patent No. US20020022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-09-897-465-12
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Query Match          95.2%; Score 99; DB 10; Length 16;
Best Local Similarity 93.8%; Pred. No. 4.3e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 1 GCCSLPPCALNNDPDC 16
DB 1 GCCSLPPCALNNDPDC 16
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RESULT 4
US-09-897-465-11
; Sequence 11, Application US/09897465
; Patent No. US20020022715A1
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; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: N11S derivative
US-09-897-465-11
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Query Match          90.4%; Score 94; DB 10; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.9e-06;
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OY 1 GCCSLPPCALNNDPDC 16
DB 1 GCCSLPPCALNNDPDC 16
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RESULT 5
; Sequence 5, Application US/09897465
; Patent No. US20020022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus aulicus
US-09-897-465-5
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Query Match          71.2%; Score 74; DB 10; Length 16;
Best Local Similarity 68.8%; Pred. No. 0.00066;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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OY 1 GCCSLPPCALNNDPDC 16
DB 1 GCCSLPPCALNNDPDC 16
```

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RESULT 6
US-09-897-465-6
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```

; Sequence 6, Application US/09897465
; Patent No. US20020022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tyr derivative
; OTHER INFORMATION: of C. aulicus AUIA
US-09-897-465-6

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Query Match          71.2%; Score 74; DB 10; Length 17;
Best Local Similarity 68.8%; Pred. No. 0.00069;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 GCCSLPPCALNPDYC 16
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DB 2 GCCSYPCFATNSDYC 17

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RESULT 7
US-09-897-465-8
; Sequence 8, Application US/09897465
; Patent No. US20020022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus aulicus
US-09-897-465-8

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Query Match          64.4%; Score 67; DB 10; Length 16;
Best Local Similarity 62.5%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 GCCSLPPCALNPDYC 16
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DB 1 GCCSYPCFATNSDYC 16

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RESULT 8
US-09-897-465-7
; Sequence 7, Application US/09897465
; Patent No. US20020022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Conus aulicus
US-09-897-465-7

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Query Match          55.8%; Score 58; DB 10; Length 15;
Best Local Similarity 64.3%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 GCCSLPPCALNPD 14
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DB 1 GCCSYPCFATNSD 14

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RESULT 9
US-09-897-465-2
; Sequence 2, Application US/09897465
; Patent No. US20020022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus magus
US-09-897-465-2

```

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Query Match          48.1%; Score 50; DB 10; Length 16;
Best Local Similarity 50.0%; Pred. No. 0.075;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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```

QY 1 GCCSLPPCALNPDYC 16
    ||||| |||
DB 1 GCCSNPCHLEHSNLC 16

```

RESULT 10

US-09-897-465-3
Sequence 3, Application US/09897465
Patent No. US20020022715A1
GENERAL INFORMATION:
APPLICANT: Oliveira, Balomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Sign
TITLE OF INVENTION: University of Utah Research Foundation
FILE REFERENCE: Uses of Alpha-Conotoxin Peptides
CURRENT APPLICATION NUMBER: US/09/897,465
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Tyr derivative
US-09-897-465-3

Query Match 48.1%; Score 50; DB 10; Length 17;
Best Local Similarity 50.0%; Pred. No. 0.79;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 GCCSLPPCALNPDYC 16
DB 2 GCCSNPVCHEHSNLC 17

RESULT 11
US-09-864-761-47370
Sequence 47370, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aegonics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47370
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL137225.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.54
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.45
US-09-864-761-47370

Query Match 45.2%; Score 47; DB 10; Length 52;
Best Local Similarity 46.7%; Pred. No. 5;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 2 CCSLPPCALNPDYC 16
DB 33 CCSPPSSLSIPLPC 47

RESULT 12
US-10-116-064-3
Sequence 3, Application US/10116064
Patent No. US20020115187A1
GENERAL INFORMATION:
APPLICANT: GREENE, JOHN M
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
METALLOPROTEINASE-4
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/116,064
FILING DATE: 05-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/262,087
FILING DATE: 04-MAR-1999
APPLICATION NUMBER: PCT/US94/14498
FILING DATE: 13-FEB-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid

; CURRENT FILING DATE: 2001-09-20
 ; PRIOR APPLICATION NUMBER: USSN 60/208,427
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 2125
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1022
 ; LENGTH: 97
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-867-550-1022

Query Match 40.9%; Score 42.5; DB 10; Length 97;
 Best Local Similarity 47.4%; Pred. No. 33;
 Matches 9; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 1 GCCSLPPCAL-----NNPD 14
 | | | | | | | | | |
 Db 68 GACRLPLCSLGERGNGPD 86

Search completed: January 8, 2003, 15:36:37
 Job time : 8.27273 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 15:27:14 ; Search time 13.0909 Seconds
(without alignments)
117,498 Million cell updates/sec

Title: US-09-897-465-10
Perfect score: 104
Sequence: 1 GCCSLPPCALNNDYC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR-73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	95.2	16	2	A54877
2	99	95.2	16	2	A54877
3	79	76.0	16	2	A59042
4	74	71.2	16	2	A59045
5	67	64.4	16	2	C59045
6	58	55.8	15	2	B59045
7	57	54.8	14	1	B69073
8	53	51.0	17	2	T36798
9	52	50.0	26	2	T23033
10	51	49.0	38	2	A12152
11	50	48.1	16	2	A59046
12	50	48.1	18	1	A58589
13	49	47.1	49	2	T43745
14	49	47.1	49	2	T43745
15	48	46.2	25	2	T16342
16	48	46.2	104	2	A26838
17	47	45.2	194	2	A38203
18	47	45.2	196	1	A38624
19	47	45.2	220	1	A37128
20	47	45.2	220	1	J06683
21	47	45.2	220	1	A55683
22	47	45.2	220	1	A55966
23	47	45.2	220	1	I53415
24	47	45.2	317	2	H97143
25	46	44.2	148	2	B82503
26	46	44.2	151	2	A83038
27	46	44.2	177	2	F98247
28	46	44.2	1101	2	T16840
29	45	43.3	156	2	B83361

30	45	43.3	388	2	T43019	probable DNA-bind
31	45	43.3	435	2	A56704	regulatory protein
32	44	42.3	553	2	G83866	hypothetical prote
33	44	42.3	716	2	U01366	polypeptidase - hepa
34	44	42.3	716	2	AG2446	single-stranded DN
35	44	42.3	1097	2	T40678	hypothetical prote
36	43.5	41.8	354	2	S60242	cinamyl-alcohol d
37	43.5	41.8	367	2	T02767	cinamyl-alcohol d
38	43.5	41.8	367	2	T02990	cinamyl-alcohol d
39	43.5	41.8	468	2	H70201	UDP-N-acetylmutam
40	43.5	41.8	2476	2	T34022	zonadhesin - pig
41	43	41.3	47	2	F81118	hypothetical prote
42	43	41.3	179	2	T19557	hypothetical prote
43	43	41.3	194	2	JC7292	flavonoidoxin FLR I
44	43	41.3	197	2	E84606	probable WRKY-type
45	43	41.3	345	2	AB1813	hypothetical prote

ALIGNMENTS

RESULT 1

A54877 alpha-conotoxin Pn1a [validated] - cone shell (Conus pennaceus)

N:Alternate names: alpha-CTX-Pn1a

C:Species: Conus pennaceus

C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000

C:Accession: A54877

R:Palnliber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zl

Biochemistry 33, 9523-9529, 1994

A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine r

A:Reference number: A54877; PMID:94347719; PMID:8068627

A:Accession: A54877

A:Molecule type: protein

A:Residues: 1-16 <FAI>

R:Hu, S.H.; Gehrmann, J.; Gudaat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.

submitted to the Brookhaven Protein Data Bank, January 1996

A:Reference number: A66355; PDB:1PEN

A:Contents: annotation: X-ray crystallography, 1.1 angstroms; residues 1-16

C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F;2-8-3-16/disulfide bonds; #status experimental

F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 95.2% Score 99; DB 2; Length 16;

Best Local Similarity 93.8% Pred. No. 3.6e-07;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNNDYC 16
Db 1 GCCSLPPCALNNDYC 16

RESULT 2

B54877 alpha-conotoxin Pn1b - cone shell (Conus pennaceus)

C:Species: Conus pennaceus

C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-May-1997

C:Accession: B54877

R:Palnliber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zl

Biochemistry 33, 9523-9529, 1994

A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine r

A:Reference number: A54877; PMID:94347719; PMID:8068627

A:Accession: B54877

A:Molecule type: protein

A:Residues: 1-16 <FAI>

C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F;2-8-3-16/disulfide bonds; #status experimental

F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 95.2%; Score 99; DB 2; Length 16;
 Best Local Similarity 93.8%; Pred. No. 3.6e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNPDYC 16
 DB 1 GCCSLPPCALNPDYC 16

RESULT 3

A59042

alpha-conotoxin Epi - cone shell (Conus episcopus)

C:Species: Conus episcopus (bishop's cone)

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 13-Aug-1999

C:Accession: A59042

R:Loughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, B.

J. Biol. Chem. 273, 15667-15674, 1998

A:Title: Alpha-conotoxin Epi, a novel sulfated peptide from Conus episcopus that select

A:Reference number: A59042; MUID:9828307; PMID:9624161

A:Accession: A59042

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <LUD>

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro

F:1-16/Product: alpha-conotoxin Epi #status experimental <MAT>

F:2-8,3-16/Disulfide bonds: #status experimental

F:15/Binding site: sulfate (Tyr) (covalent) #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 76.0%; Score 79; DB 2; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.00017;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNPDYC 16
 DB 1 GCCSLPPCALNPDYC 16

RESULT 4

A59045

alpha-conotoxin AuiA - cone shell (Conus aulicus)

C:Species: Conus aulicus (court cone)

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C:Accession: A59045

R:Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McI

J. Neurosci. 18, 8571-8579, 1998

A:Title: Alpha-conotoxin AuiB selectively blocks alpha3beta4 nicotinic acetylcholine rec

A:Reference number: A59045; MUID:99003392; PMID:9786965

A:Accession: A59045

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <LUD>

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro

F:1-16/Product: alpha-conotoxin AuiA #status experimental <MAT>

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 71.2%; Score 74; DB 2; Length 16;
 Best Local Similarity 68.8%; Pred. No. 0.0008;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNPDYC 16
 DB 1 GCCSLPPCALNPDYC 16

RESULT 5

C59045

alpha-conotoxin AuiC - cone shell (Conus aulicus)

C:Species: Conus aulicus (court cone)

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C:Accession: C59045

R:Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.;

J. Neurosci. 18, 8571-8579, 1998

A:Title: Alpha-conotoxin AuiB selectively blocks alpha3beta4 nicotinic acetylcholine

A:Reference number: A59045; MUID:99003392; PMID:9786965

A:Accession: C59045

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <LUD>

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F:1-16/Product: alpha-conotoxin AuiC #status experimental <MAT>

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 64.4%; Score 67; DB 2; Length 16;
 Best Local Similarity 62.5%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNPDYC 16
 DB 1 GCCSLPPCALNPDYC 16

RESULT 6

B59045

alpha-conotoxin AuiB - cone shell (Conus aulicus)

C:Species: Conus aulicus (court cone)

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C:Accession: B59045

R:Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.;

J. Neurosci. 18, 8571-8579, 1998

A:Title: Alpha-conotoxin AuiB selectively blocks alpha3beta4 nicotinic acetylcholine

A:Reference number: A59045; MUID:99003392; PMID:9786965

A:Accession: B59045

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <LUD>

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F:1-15/Product: alpha-conotoxin AuiB #status experimental <MAT>

F:2-8,3-15/Disulfide bonds: #status experimental

F:15/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 55.8%; Score 58; DB 2; Length 15;
 Best Local Similarity 64.3%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNPD 14
 DB 1 GCCSLPPCALNPD 14

RESULT 7

E69073

NADP-reducing hydrogenase (EC 1.-.-.-) chain A - Methanobacterium thermoautotrophicum

C:Species: Methanobacterium thermoautotrophicum

C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Oct-2000

C:Accession: E69073

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T

; Qu, D.; Spadafora, R.; Vicare, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jivani,

K.I.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: E69073

A:Status: preliminary

A:Molecule type: nucleic acid sequence not shown; translation not shown

A:Residues: 1-149 <MTH>

A:Cross-references: GB:AE000915; GB:AE000666; NID:g2622664; PIDN:AAB6022.1; PID:g262

C:Experimental source: strain Delta H

A:Gene: MTH1548

C:Superfamily: NADH dehydrogenase (ubiquinone) I chain E; NADH dehydrogenase (ubiquinone)
 C:Keywords: 2Fe-2S; iron-sulfur protein; metalloprotein; NADP; oxidoreductase
 F:9-148/Domain: NADH dehydrogenase (ubiquinone) I chain E homology <NO>
 F:75,80,116,120/binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 54.8%; Score 57; DB 1; Length 149;
 Best Local Similarity 64.3%; Pred. No. 0.93;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNMPD 14
 ||||| ||| : :
 Db 118 GCCSLAPCAMVND 131

RESULT 8

T36798
 probable transcription regulator soxR-like - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999

R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, July 1999

A:Accession: T36798
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-175

A:Cross-references: EMBL:AL096811; PIDN:CA846795.1; GSPDB:GN00070; SCOEDB:SCI30A.18C

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCI30A.18C

Query Match 51.0%; Score 53; DB 2; Length 175;
 Best Local Similarity 64.3%; Pred. No. 3.7;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNMPD 14
 ||||| ||| : :
 Db 122 GCLSLFECVLSNP 135

RESULT 9

T23033
 hypochemical protein H02K04.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T23033; T27666
 R:White, S.

submitted to the EMBL Data Library, June 1998
 A:Reference number: Z19657

A:Accession: T23033

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-260 <W1>

A:Cross-references: EMBL:AL023813; PIDN:CA19425.1; GSPDB:GN00023; CESP:H02K04.1

A:Experimental source: clone H02K04

R:Basham, V.
 submitted to the EMBL Data Library, October 1996

A:Reference number: Z20401

A:Accession: T27666

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-260 <W1>

A:Cross-references: EMBL:Z81142; PIDN:CA803511.1; GSPDB:GN00023; CESP:H02K04.1

A:Experimental source: clone ZK1037

OY 3 GCLPPCALNPDYC 16
 | : ||||| : : |
 Db 102 CAAPPCAVTDPPVC 115

RESULT 10

hypothetical protein all2776 [imported] - Nostoc sp. (strain PCC 7120)

A:Accession: A12152

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: A12152

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Iriku

Nakazaki, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata

DNA Res. 8, 205-213, 2001

A:Title: Complete genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: A12152

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-386 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA874475.1; PID:q17131869; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all2776

Query Match 49.0%; Score 51; DB 2; Length 386;
 Best Local Similarity 50.0%; Pred. No. 13;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 GCLPPCALNPDYC 16
 ||||| ||| : : |
 Db 108 CAAPPCAVTDPPVC 121

RESULT 11

A59046
 alpha-conotoxin MII - cone shell (Conus magus)

C:Species: Conus magus (magus cone)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: A59046

R:Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.

J. Biol. Chem. 271, 7522-7528, 1996

A:Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine rece

A:Reference number: A59046; MUID:96205934; PMID:8631783

A:Accession: A59046

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <CAR>

A:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F:1-16/Product: alpha-conotoxin MII #status experimental <MAT>

F:2-8-3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 48.1%; Score 50; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.3;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNPDYC 16
 ||||| ||| : : |
 Db 1 GCCSNPVCHLSNMLC 16

RESULT 12

A58589
 alpha-conotoxin EI - cone shell (Conus ermineus)

C:Species: Conus ermineus (ermine cone)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A58589

R:Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craib, A.G.; Groebe, D.R.; Abramson, S.N

Biochemistry 34, 14519-14526, 1995

A:Title: alpha-Conotoxin FI, a new nicotinic acetylcholine receptor antagonist with novel
 A:Reference number: A58589; MID:96062516; PMID:7578057
 A:Accession: A58589
 A:Molecule type: protein
 A:Residues: 1-18 <MAR>
 A:Note: sequence confirmed by chemical synthesis
 C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic
 C:Superfamily: alpha-conotoxin
 C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pos
 F:3/Modified site: 4-hydroxyproline (Pro) #status experimental
 F:4-10/5-18/Disulfide bonds: #status experimental
 F:18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 48.1%; Score 50; DB 1; Length 18;
 Best Local Similarity 46.7%; Pred. No. 1.4;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 CCSPCALNPDYC 16
 DB 4 CCYHPTCNMSNPQIC 18
 ||| |::||| |

RESULT 13
 T43745
 clr4 protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
 C:Accession: T43745
 R:Rivanova, A.V.; Bonaduce, M.; Ivanov, S.V.; Klar, A.J.S.
 Nature Genet. 19, 192-195, 1998
 A:Title: Chromo- and SET domains of the Clr4 protein are essential for silencing in fission
 A:Reference number: 222657; MID:98282102; PMID:9620780
 A:Accession: T43745
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-490 <IVA>
 A:Cross-references: EMBL:AF061854; PIDN:AAC18302.1
 C:Genetics:
 A:Gene: clr4
 A:Map position: II
 C:Function:
 A:Description: required for silencing of the mating-type locus and centromeres

Query Match 47.1%; Score 49; DB 2; Length 490;
 Best Local Similarity 60.0%; Pred. No. 29;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CCSPCALNPDYC 16
 DB 262 CSSLGGCDLNPSRC 276
 ||| |::||| |

RESULT 14
 T43700
 mating-type loci and centromere silencing protein clr4 - fission yeast (Schizosaccharomyces
 C:Species: Schizosaccharomyces pombe
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
 C:Accession: T43700; T40460
 R:Lord, P.
 submitted to the EMBL Data Library, July 1998
 A:Reference number: 222635
 A:Accession: T43700
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-490 <LOR>
 A:Cross-references: EMBL:AJ007840; PIDN:CAA07709.1
 A:Experimental source: strain sp 813
 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
 submitted to the EMBL Data Library, November 1998
 A:Reference number: 221931
 A:Accession: T40460
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-490 <LYN>
 A:Cross-references: EMBL:AL034382; PIDN:CAA22283.1; GSPDB:GN00067; SPDB:SPBC428.08C
 A:Experimental source: strain 972h-; cosmid c428
 C:Genetics:
 A:Gene: clr4; SPBC428.08C
 A:Map position: 2
 C:Function:
 A:Description: essential for silencing of centromeres and the mating-type loci

Query Match 47.1%; Score 49; DB 2; Length 490;
 Best Local Similarity 60.0%; Pred. No. 29;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CCSPCALNPDYC 16
 DB 262 CSSLGGCDLNPSRC 276
 ||| |::||| |

RESULT 15
 T16342
 hypothetical protein F42C5.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T16342
 R:Du, Z.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid F42C5.
 A:Reference number: Z18497
 A:Accession: T16342
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-250 <DUZ>
 A:Cross-references: EMBL:U00799; NID:g1065935; PID:g1065941; PIDN:AAA81484.1; CESP:F4
 C:Genetics:
 A:Gene: CESP:F42C5.7
 A:Introns: 15/2; 40/3; 167/3; 191/3

Query Match 46.2%; Score 48; DB 2; Length 250;
 Best Local Similarity 50.0%; Pred. No. 23;
 Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 1 GCCSL--PCALNPDYC 16
 DB 61 GCCSMGPPPPPPPPMC 78
 ||| |::||| |

Search completed: January 8, 2003, 15:30:29
 Job time: 15.0909 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 15:24:24 ; Search time 7.27273 Seconds
(without alignments)
91.248 Million cell updates/sec

Title: US-09-897-465-10
Perfect score: 104
Sequence: 1 GCCSLPPCALINPDYC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	95.2	16	1	CXAA_CONPE
2	99	95.2	16	1	CXAB_CONPE
3	79	76.0	16	1	CXAL_CONEP
4	74	71.2	16	1	CXAL_CONEP
5	67	64.4	16	1	CXAL_CONEP
6	66	63.5	15	1	CXAL_CONEP
7	52	50.0	16	1	CXAL_CONEP
8	50	48.1	16	1	CXAL_CONEP
9	50	48.1	16	1	CXAL_CONEP
10	49	47.1	16	1	CXAL_CONEP
11	48.5	46.6	253	1	CPH_KLEAE
12	48	46.2	1046	1	PST4_DICDI
13	47	45.2	19	1	CXR_CONTR
14	47	45.2	69	1	CXAL_CONTE
15	47	45.2	194	1	TM2_RABT
16	47	45.2	196	1	TM2_RABT
17	47	45.2	220	1	TM2_BOVIN
18	47	45.2	220	1	TM2_CANPA
19	47	45.2	220	1	TM2_CAVPO
20	47	45.2	220	1	TM2_HUMAN
21	47	45.2	220	1	TM2_MOUSE
22	47	45.2	220	1	TM2_MOUSE
23	46	44.2	91	1	VP22_BPAP
24	46	44.2	446	1	SH7_CAVPO
25	45	43.3	156	1	SOXR_PSEAE
26	44	42.3	30	1	CXVB_CONER
27	43.5	41.8	354	1	CAD1_EUCGU
28	43.5	41.8	356	1	CAD2_EUCGU
29	43.5	41.8	356	1	CADH_EUCGU
30	43.5	41.8	365	1	CADH_EUCGU
31	43.5	41.8	367	1	CADH_EUCGU
32	43.5	41.8	468	1	MURC_BORBU
33	43.5	41.8	2476	1	ZAN_PLG

34	43	41.3	177	1	P111_HUMAN
35	43	41.3	194	1	FLR_DESGI
36	43	41.3	224	1	TM2_RAT
37	43	41.3	350	1	FX32_RAT
38	43	41.3	355	1	FX32_HUMAN
39	43	41.3	355	1	FX32_MOUSE
40	43	41.3	488	1	H1X1_HUMAN
41	43	41.3	730	1	ROM_HUMAN
42	42.5	40.9	355	1	CADH_EUCGU
43	42.5	40.9	361	1	CADH_EUCGU
44	42.5	40.9	365	1	CADH_EUCGU
45	42.5	40.9	1277	1	IF3X_YEAST

ALIGNMENTS

RESULT 1	CXAA_CONPE	STANDARD;	PRT;	16 AA.
AC	P50984:			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Alpha-conotoxin Pn1A.			
OS	Conus pennaceus (Feathered cone).			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;			
OC	Neogastropoda; Conoidea; Conidae; Conus.			
ON	NCBI_TaxID=37335;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RX	MEDLINE=94347719: PubMed=8068627;			
RA	Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,			
RA	Spira M.E., Zlotkin E.,			
RT	"New mollusc-specific alpha-conotoxins block Aplysia neuronal			
RT	acetylcholine receptors."			
RL	Biochemistry 33:9523-9529(1994).			
RN	[2]			
RP	SULFATION OF TYR-15.			
RX	MEDLINE=99242956; PubMed=10226369;			
RA	Wolfe J.L., Chu F., Ball H., Wolfe J.L., Fainzilber M.,			
RA	Baldwin M.A., Burlingame A.L.,			
RT	"Identification of tyrosine sulfation in Conus pennaceus conotoxins			
RT	alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and			
RT	phosphopeptides by electrospray, matrix-assisted laser			
RT	desorption/ionization (MALDI) and atmospheric pressure MALDI mass			
RT	spectrometry."			
RL	J. Mass Spectrom. 34:447-454(1999).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).			
RX	MEDLINE=96311277; PubMed=8740364;			
RA	Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,			
RA	Martin J.L.,			
RT	"The 1.1 A crystal structure of the neuronal acetylcholine receptor			
RT	antagonist, alpha-conotoxin Pn1A from Conus pennaceus."			
RL	Structure 4:417-423(1996).			
CC	-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY			
CC	BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS			
CC	INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE			
CC	SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS			
CC	PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.			
CC	-1- TISSUE SPECIFICITY: Expressed by the venom duct.			
CC	-1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE			
CC	FAMILY.			
DR	PDB; 1PBN; 21-APR-97.			
KW	postsynaptic neurotoxin; Neurotoxin; Toxin;			
KW	acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.			
FT	DISULFID 2 8			
FT	DISULFID 3 16			
FT	MOD_RES 15 15			
FT	MOD_RES 16 16			
FT	MOD_RES 16 16			
FT	SULFATION.			
FT	AMIDATION.			

SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match 95.2%; Score 99; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 2.7e-08; Mismatches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNNDYC 16
Db 1 GCCSLPPCALNNDYC 16

RESULT 2

CMAB_COMPE
ID CMAB_COMPE STANDARD; PRT; 16 AA.
AC P50985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin PnIB.
OS Conus pennaculus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
ON NCBI_TaxID=37335;

SEQUENCE:
RP TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block *Aplysia* neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN [2]

SULFATION OF TYR-15.
RP MEDLINE=99242956; PubMed=10226369;
RX Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT Identification of tyrosine sulfation in *Conus pennaculus* conotoxins
RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
RT phosphorylation by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]

X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=97444322; PubMed=9289511;
RA Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
RT "Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB:
RT comparison with alpha-conotoxins PnIA and GI.";
RL Biochemistry 36:11323-11330(1997).

-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.

PDB: 1AKG; 20-MAY-98.
DR Postsynaptic neurotoxin; Neurotoxin; Toxin;
KM Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT MOD_RES 3 16
FT MOD_RES 15 15
FT MOD_RES 16 16
SQ SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;

Query Match 95.2%; Score 99; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.7e-08;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNNDYC 16

Db 1 GCCSLPPCALNNDYC 16

RESULT 3

CMAB_COMPE
ID CMAB_COMPE STANDARD; PRT; 16 AA.
AC P56638;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Epi.
OS Conus episcopatus (Bishop's cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
ON NCBI_TaxID=88764;

X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=98376423; PubMed=9708977;
RA Hu S.H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,
RA Alewood P.F., Lewis R.J., Martin J.L.;
RT "The 1.1-A resolution crystal structure of [Tyr15]Epi, a novel
RT alpha-conotoxin from *Conus episcopatus*, solved by direct methods.";
RL Biochemistry 37:11425-11433(1998).

-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 AND ALPHA-
CC 3/BETA-4 SUBUNITS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.

PDB: 1AOM; 13-JAN-99.
DR Postsynaptic neurotoxin; Neurotoxin; Toxin;
KM Acetylcholine receptor inhibitor; Amidation;
KW Sulfation; 3D-structure.
FT DISULFID 2 8
FT MOD_RES 3 16
FT MOD_RES 15 15
FT MOD_RES 16 16
SQ SEQUENCE 16 AA; 1792 MW; C63385F37C99B4C CRC64;

Query Match 76.0%; Score 79; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.8e-05;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNNDYC 16
Db 1 GCCSLPPCALNNDYC 16

RESULT 4

CMAB_COMPE
ID CMAB_COMPE STANDARD; PRT; 16 AA.
AC P56639;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin AURA.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
ON NCBI_TaxID=89437;

SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP TISSUE=Venom;
RX MEDLINE=99003392; PubMed=9786965;
RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
RA Oliveira B.M., McIntosh J.M.;
RT "Alpha-conotoxin AURA selectively blocks alpha3 beta4 nicotinic
RT acetylcholine receptors and nicotine-evoked norepinephrine release.";
RL J. Neurosci. 18:8571-8579(1998).

CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR HSP: P50984; 1PEN.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 16 16
 SQ SEQUENCE 16 AA; 1731 MW; 1E310EBB8FDC7001 CRC64;
 Query Match 71.2%; Score 74; DB 1; Length 16;
 Best Local Similarity 68.8%; Pred. No. 8.9e-05;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 5

CCX3_CONAL ID CX3_CONAL STANDARD; PRT; 16 AA.
 AC P56641;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Auitc.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_Taxid=89437;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE-Venom;
 RX MEDLINE=99003392; PubMed=9786965;
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
 RA Olivera B.M., McIntosh J.M.;
 RT "Alpha-conotoxin Auitc selectively blocks alpha3 beta4 nicotinic
 RT acetylcholine receptors and nicotine-evoked norepinephrine release.";
 RL J. Neurosci. 18:8571-8579(1998).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1667.6; METHOD=Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR HSP: P50984; 1PEN.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 16 16
 SQ SEQUENCE 16 AA; 1673 MW; 1E310DBB8FDC7001 CRC64;

Query Match 64.4%; Score 67; DB 1; Length 16;
 Best Local Similarity 62.5%; Pred. No. 0.00085;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNPDYC 16
 DB 1 GCCSYPCFATNSGYC 16

RESULT 6
 CCX2_CONAL ID CX2_CONAL STANDARD; PRT; 15 AA.
 AC P56640;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Auitc.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_Taxid=89437;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE-Venom;
 RX MEDLINE=99003392; PubMed=9786965;
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
 RA Olivera B.M., McIntosh J.M.;
 RT "Alpha-conotoxin Auitc selectively blocks alpha3 beta4 nicotinic
 RT acetylcholine receptors and nicotine-evoked norepinephrine release.";
 RL J. Neurosci. 18:8571-8579(1998).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1572.5; METHOD=Electrospray
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 8
 FT DISULFID 3 15
 FT MOD_RES 15 15
 SQ SEQUENCE 15 AA; 1578 MW; 84EF95FDC700155 CRC64;

Query Match 63.5%; Score 66; DB 1; Length 15;
 Best Local Similarity 71.4%; Pred. No. 0.0011;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNPD 14
 DB 1 GCCSYPCFATNPD 14

RESULT 7
 CCX2_CONTE ID CX2_CONTE STANDARD; PRT; 66 AA.
 AC 09XZK7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-type conotoxin Tx2 precursor.
 OS Conus textile (Cloth-of-gold cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_Taxid=6494;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Venom duct;
 RX MEDLINE=20037955; PubMed=10573284;
 RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
 RT "Conopeptides from Conus striatus and Conus textile by cDNA
 RT cloning.";
 RL Peptides 20:1139-1144(1999).
 CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 CC bind to the nicotinic acetylcholine receptors (NACHR) and thus
 CC inhibit them (BY similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF146353; AAD31913.1;
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Signal.
FT SIGNAL 1 21
FT PROPEP 22 48
FT PEPTIDE 49 66 POTENTIAL.
FT DISULFID 51 57 ALPHA-TYPE CONOTOXIN TX2.
FT DISULFID 52 65 BY SIMILARITY.
SQ SEQUENCE 66 AA; 7254 MW; EDDBS9BBAB94F26F CRC64;

Query Match 50.0%; Score 52; DB 1; Length 66;
Best Local Similarity 46.7%; Pred. No. 0.41;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 2 CCSLPPCALNPDYC 16
Db 51 CCSPACNVDPHPC 65

RESULT 8
CXA2_CONMA STANDARD; PRT; 16 AA.
ID CXA2_CONMA
AC P56636;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin MII (M2).
OS Conus magus (Mugil cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RC TISSUE-Venom;
RX MEDLINE=96205934; PubMed=8631783;
RA Carter G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
RA McIntosh J.M.;
RT "A new alpha-conotoxin which targets alphabeta2 nicotinic
RT acetylcholine receptors."
RT J. Biol. Chem. 271:7522-7528(1996).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=98062282; PubMed=9398298;
RA Shon K.-J., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;
RT "Three-dimensional solution structure of alpha-conotoxin MII, an
RT alphabeta2 neuronal nicotinic acetylcholine receptor-targeted
RT ligand."
RT Biochemistry 36:15693-15700(1997).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99060038; PubMed=9843366;
RA Hill J.M., Comen C.J., Miranda L.P., Bingham J.-P., Alewood P.F.,
RA Craik D.J.;
RT "Three-dimensional solution structure of alpha-conotoxin MII by NMR
RT spectroscopy: effects of solution environment on helicity."
RT Biochemistry 37:15621-15630(1998).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS. IT
CC HAS AN ACTIVITY 2 TO 4 ORDERS OF MAGNITUDE LESS POTENT ON OTHER
CC NACHR SUBUNIT COMBINATIONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.

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CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PDB: 1MIT; 21-OCT-98.
DR PDB: 1M2C; 13-JAN-99.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 16 16
SQ SEQUENCE 16 AA; 1716 MW; 282AEF190166CAF9 CRC64;

Query Match 48.1%; Score 50; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 0.21;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GCCSLPPCALNPDYC 16
Db 1 GCCSNPVCLEHSLNC 16

RESULT 9
CXA1_CONER STANDARD; PRT; 18 AA.
ID CXA1_CONER
AC P50982;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin EI.
OS Conus ermineus (Atlantic fish-hunting cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=55423;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=96062516; PubMed=7578057;
RA Martinez J.S., Olivera B.M., Gray W.R., Craig A.G., Groebe D.R.,
RA Abramson S.N., McIntosh J.M.;
RT "Alpha-conotoxin EI, a new nicotinic acetylcholine receptor
RT antagonist with novel selectivity."
RT Biochemistry 34:14519-14526(1995).
RN [2]
RP FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
RP BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
RP INHIBIT THEM.
CC -1- SUBUNIT: Binds nicotinic acetylcholine receptor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Hydroxylation.
FT DISULFID 4 10
FT DISULFID 5 18
FT MOD_RES 3 3
FT MOD_RES 18 18
SQ SEQUENCE 18 AA; 2082 MW; 60A61A6C427A6B5E CRC64;

Query Match 48.1%; Score 50; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 0.23;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 CCSLPPCALNPDYC 16
Db 4 CCYHPCNMSPQIC 18

RESULT 10
CIR4_SCHPO STANDARD; PRT; 490 AA.
ID CIR4_SCHPO
AC 060016; 074565;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

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DE Cryptic local regulator 4.
 GN CUB4 OR SPBC428.08C.
 OS Schizosaccharomyces pombe (fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 ON NCBI_TaxId=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96282102; PubMed=9620780;
 RA Ivanova A.V., Bonaduce M.J., Ivanov S.V., Klar A.J.S.;
 RT "The chromo and SET domains of the Ctr4 protein are essential for
 silencing in fission yeast."
 RL Nat. Genet. 19:192-195(1998).
 RP SEQUENCE FROM N.A.
 RC STRAIN=SP 813;
 RA Lord P.;
 RL Thesis (1998), University of Edinburgh, U.K.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor J., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Gymnopreze B.,
 RA Welljens I., Volscheit E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Delaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerruti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
 RA Spakovski G.V., Ussery D., Bartell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: ESSENTIAL FOR SILENCING OF CENTROMERES AND DIRECTIONAL
 SWITCHING OF THE MATING TYPE. ACTS THROUGH THE ORGANIZATION OF
 REPRESSIVE CHROMATIN STRUCTURE.
 CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE SVAR3-9 FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 CHROMO DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SET DOMAIN.
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 CC -----
 DR EMBL: AF061854; AAC18302.1; -;
 DR EMBL: AJ007840; CAA07709.1; -;
 DR EMBL: AL034382; CAA22283.1; -;
 DR InterPro: IPR000953; Chromo.
 DR InterPro: IPR003616; PostSET.
 DR InterPro: IPR001214; SET.
 DR InterPro: IPR003606; Zn2-binding.
 DR Pfam: PF00385; chromo; 1.

DR Pfam: PF00856; SET; 1.
 DR SMART: SM00298; CHROMO; 1.
 DR SMART: SM00508; PostSET; 1.
 DR SMART: SM00468; PreSET; 1.
 DR SMART: SM00317; SET; 1.
 DR PROSITE: PS00598; CHROMO_1; 1.
 DR PROSITE: PS0013; CHROMO_2; 1.
 DR PROSITE: PS0280; SET; 1.
 DR Nuclear protein; Chromatin regulator.
 KW DOMAIN 8 59
 FT DOMAIN 339 456
 FT SET.
 FT CONFLICT 19 19 D -> G (IN REF. 1).
 FT CONFLICT 437 437 A -> G (IN REF. 1).
 FT SEQUENCE 490 AA; 55918 MW; 53C3EC87BCBA51FF CRC64;
 SO
 Query Match 47.1%; Score 49; DB 1; Length 490;
 Best Local Similarity 60.0%; Pred. No. 7.2;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 2 CCSLPPCALNPDYC 16
 DB 262 CSSLGCDLNNPSRC 276
 RESULT 11
 ID GPH_KLEAE STANDARD; PRT; 253 AA.
 AC 09EY15;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphoglycolate phosphatase (EC 3.1.3.18) (PGP).
 GN GPH.
 OS Klebsiella aerogenes.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Klebsiella.
 OX NCBI_TaxId=28451;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M70;
 RX MEDLINE=20566700; PubMed=11114933;
 RA Kolko M.M., Kapetanovich L.A., Lawrence J.G.;
 RT "Alternative pathways for siroheme synthesis in Klebsiella
 aerogenes."
 RL J. Bacteriol. 183:328-335(2001).
 CC -1- CATALYTIC ACTIVITY: 2-phosphoglycolate + H(2)O = glycolate +
 phosphate.
 CC -1- SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEH FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF308467; AAG42459.1; -;
 DR InterPro: IPR001454; Hlgnase/hydriase.
 DR Pfam: PF00702; Hydrolase; 1.
 DR PRINTS: PR00413; HADHALOGNASE.
 KW Carbohydrate metabolism; Hydrolase.
 SO SEQUENCE 253 AA; 27452 MW; DFC02F853188F01D CRC64;
 SO
 Query Match 46.6%; Score 48.5; DB 1; Length 253;
 Best Local Similarity 41.7%; Pred. No. 4.5;
 Matches 10; Conservative 2; Mismatches 3; Indels 9; Gaps 1;
 OY 1 GCCSL-----PCALNPDY 15
 DB 205 CCCSVGLTYGYNVEPLALSEPDI 228

RESULT 12
PSTA_DICDI STANDARD; PRT: 1046 AA.
AC P11976;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prestalk protein precursor.
GN ECMB.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
RX MEDLINE-88015608; PubMed-3658700;
RA Ceccarelli A., McRobbie S.J., Jermyn K.A., Duffy K., Early A.,
Williams J.G.;
RT "Structural and functional characterization of a Dictyostelium gene
encoding a DIF inducible, prestalk-enriched mRNA sequence.";
RL Nucleic Acids Res. 15:7463-7476(1987).
RN [2]
RP SEQUENCE OF 1-17 FROM N.A.
RX MEDLINE-87257883; PubMed-3600646;
RA Ayres K., Newman W., Roweckamp W.G., Chung S.;
RT "Developmental regulation of Dnase I-hypersensitive sites in
Dictyostelium discoideum.";
RL Mol. Cell. Biol. 7:1823-1829(1987).
CC -1- INDUCTION: BY THE PUTATIVE STALK-SPECIFIC MORPHOGEN DIF
(DIFFERENTIATION INDUCING FACTOR).
CC -1- SIMILARITY: THE REPEATED SEQUENCES ARE HIGHLY HOMOLOGOUS TO A
REPEAT OF THE PDD63 MRNA OF DICTYOSTELIUM DISCOIDEUM.
CC -----
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CC -----
DR EMBL: M16345; AAA3216.1; -
DR PTR: A26838; A26838.
DR HSSP: P15445; 1A3F.
DR DictyDb; DD03006; ecmb.
DR InterPro; IPR001673; S_mold_repeat.
DR Pfam; PF00526; S_mold_repeat; 42.
DR ProDom; PD006869; S_mold_repeat; 8.
KW Signal; Repeat.
FT CHAIN 1 18 PROBABLE.
FT DOMAIN 31 1012 PRESTALK PROTEIN.
FT REPEAT 31 53 41 X 24 AA TANDEM REPEATS, CYS-RICH.
FT REPEAT 54 77 X-1.
FT REPEAT 78 101 X-2.
FT REPEAT 102 125 X-3.
FT REPEAT 126 149 A-1.
FT REPEAT 150 173 A-2.
FT REPEAT 174 197 A-3.
FT REPEAT 198 221 A-4.
FT REPEAT 222 245 A-5.
FT REPEAT 246 269 A-6.
FT REPEAT 270 293 A-7.
FT REPEAT 294 317 A-8.
FT REPEAT 318 341 A-9.
FT REPEAT 342 365 A-10.
FT REPEAT 366 389 A-11.
FT REPEAT 390 413 A-12.
FT REPEAT 414 437 A-9.
FT REPEAT 438 461 A-10.
FT REPEAT 462 485 A-11.
FT REPEAT 486 509 A-12.
FT REPEAT 510 533 B-6.

FT REPEAT 534 557 A-13.
FT REPEAT 558 581 A-4.
FT REPEAT 582 605 A-14.
FT REPEAT 606 629 A-15.
FT REPEAT 630 653 A-16.
FT REPEAT 654 677 B-7.
FT REPEAT 678 701 A-17.
FT REPEAT 702 725 A-18.
FT REPEAT 726 749 B-8.
FT REPEAT 750 773 A-19.
FT REPEAT 774 797 A-20.
FT REPEAT 822 845 A-21.
FT REPEAT 846 869 A-22.
FT REPEAT 870 893 A-23.
FT REPEAT 894 917 B-10.
FT REPEAT 918 941 A-24.
FT REPEAT 942 964 A-25.
FT REPEAT 965 988 A-26.
FT REPEAT 989 1012 A-27.
SQ SEQUENCE 1046 AA; 108823 MW; F9D6C04FD7D85818 CRC64;

Query Match 46.2%; Score 48; DB 1; Length 1046;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GCSLPPCALNNPDYC 16
DB 41 GCSNTPTININDDEC 56

RESULT 13

ID CXR-CONTU STANDARD; PRT: 19 AA.
AC P36811;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rho-conotoxin T1A (Rho-T1A).
OS Conus tulipa (Fish-hunting cone snail) (Tulip cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
CC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6495;
RN [1]
RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
RC TISSUE=Venom.
RX MEDLINE-21419681; PubMed-11528421;
RA Sharpe T.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
RA Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
RA Lewis R.J.;
RT "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
noradrenaline transporter.";
FT NADRENALINE TRANSPORTER.
FT Nat. Neurosci. 4:902-907(2001).
CC -1- FUNCTION: Inhibits alpha-1 adrenergic receptors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=2390.15; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE RHO-CONOTOXIN FAMILY.
DR PDB; 1TEN; 03-APR-02.
KW Toxin; Amidation; 3D-structure.
FT DISULFID 5 11
FT MOD RES 19 19
FT MOD RES 19 19
SQ SEQUENCE 19 AA; 2396 MW; C9517DDE62CA89DC CRC64;

Query Match 45.2%; Score 47; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 0.64;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 2 GCSLPPCALNNPDYC 16
DB 5 CCLIPACRRNKKFC 19

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RESULT 14
CXAL CONTE STANDARD; PRT; 69 AA.
ID CXAL CONTE
AC 09XZK6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-type conotoxin TX1 precursor.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conidae; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom duct;
RX MEDLINE=20037955; PubMed=10573284;
RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-D.;
RT "Conopeptides from Conus striatus and Conus textile by cDNA
RT cloning."
RL Peptides 20:1139-1144(1999).
CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AF146352; AAD31912.1; -
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Signal; Amidation.
FT SIGNAL 1 21
FT PROPEP 22 48
FT PEPTIDE 49 66 ALPHA-TYPE CONOTOXIN TX1.
FT DISULFID 51 57 BY SIMILARITY.
FT DISULFID 52 65 BY SIMILARITY.
FT MOD_RES 66 66
FT SEQUENCE 69 AA; 7442 MW; E36CE90BF1B56B0 CRC64;
SQ
Query Match 45.2%; Score 47; DB 1; Length 69;
Best Local Similarity 46.7%; Pred. No. 2.2;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY 2 CCLSPCALNPDYC 16
DB 51 CCLSPCALNPDYC 65

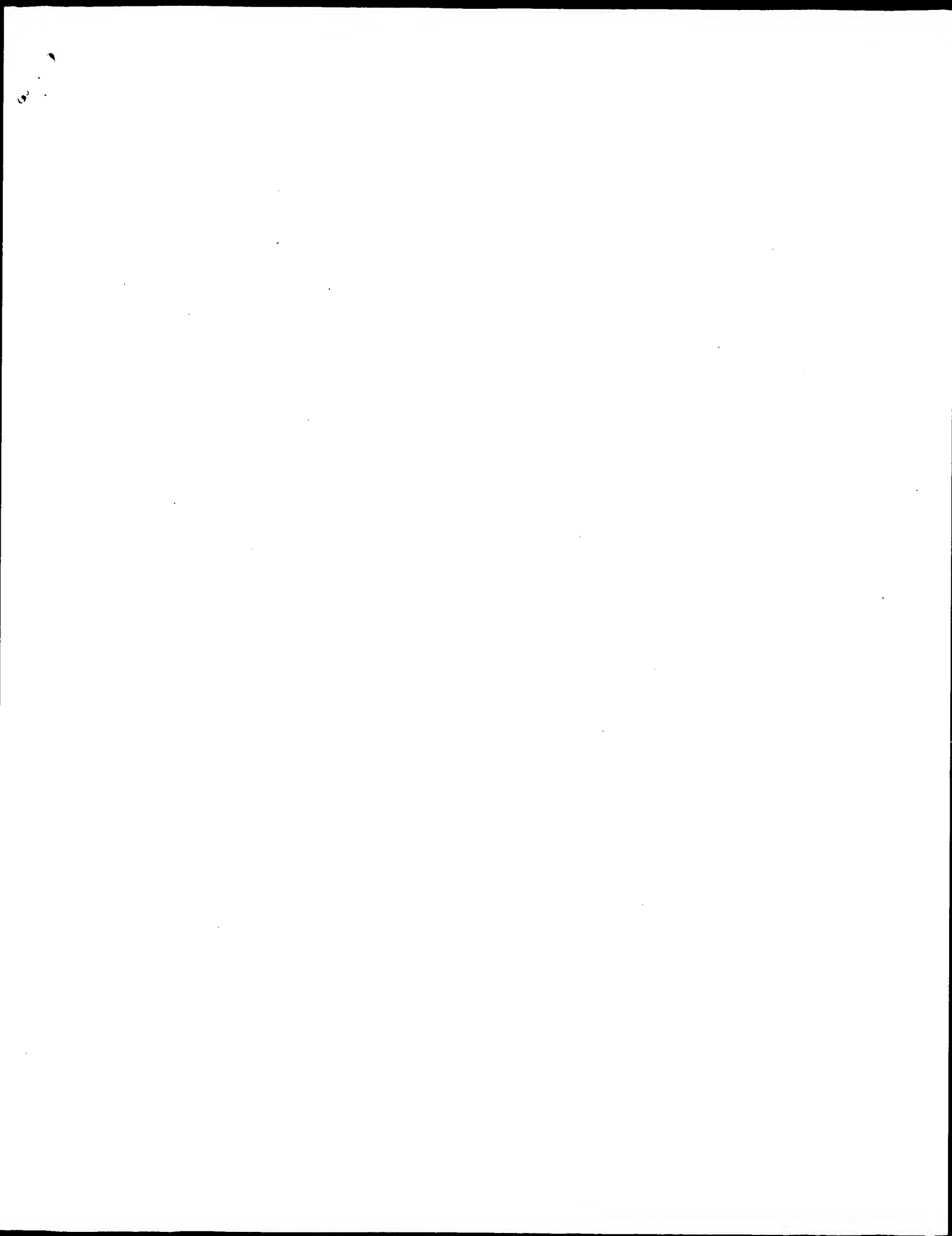
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RX MEDLINE=96049920; PubMed=8548358;
RA Wertheimer S.J., Katz S.L.;
RT "Molecular cloning and characterization of rabbit TIMP2.";
RL Inflamm. Res. 44:S121-S122(1995).
RN [2]
RP SEQUENCE OF 17-154 FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=96057575; PubMed=9837780;
RA Reno C., Boykiv R., Martinez M.L., Hart D.A.;
RT "Temporal alterations in mRNA levels for proteinases and inhibitors
RT and their potential regulators in the healing medial collateral
RT ligament.";
RL Biochem. Biophys. Res. Commun. 252:757-763(1998).
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC -----
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CC -----
DR EMBL; AF069713; AAC95005.1; -
DR HSSP; P16035; 1BR9.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Metalloprotease inhibitor.
FT DISULFID 1 72
FT DISULFID 3 101 BY SIMILARITY.
FT DISULFID 13 126 BY SIMILARITY.
FT DISULFID 128 175 BY SIMILARITY.
FT DISULFID 133 138 BY SIMILARITY.
FT DISULFID 146 167 BY SIMILARITY.
FT CONFLICT 17 17 I -> V (IN REF. 2).
FT CONFLICT 25 26 NK -> K (IN REF. 2).
FT CONFLICT 58 58 Q -> K (IN REF. 2).
FT CONFLICT 78 78 I -> V (IN REF. 2).
FT CONFLICT 93 95 NGN -> DER (IN REF. 2).
FT CONFLICT 109 109 T -> S (IN REF. 2).
FT CONFLICT 112 112 A -> S (IN REF. 2).
FT CONFLICT 131 131 T -> S (IN REF. 2).
SQ SEQUENCE 194 AA; 21849 MW; CDC8101A2D38C4A9 CRC64;
OY 1 GC-----CCLSPCALNPDYC 16
DB 125 GCECKITRCMIPCYISSPDEC 146
Query Match 45.2%; Score 47; DB 1; Length 194;
Best Local Similarity 36.4%; Pred. No. 5.7;
Matches 8; Conservative 4; Mismatches 4; Indels 6; Gaps 1;

```

Search completed: January 8, 2003, 15:28:57
 Job time : 8.27273 secs



Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 15:26:54 : Search time 23.7576 Seconds

(without alignments)
138.766 Million cell updates/sec

Title: US-09-897-465-10

Sequence: 1 GCCSLPPCALNPDYC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	95.2	61	5	Q9BP57
2	93	89.4	61	5	Q9BP56
3	57	54.8	149	17	027591
4	53	51.0	175	16	Q9S255
5	52	50.0	260	5	045933
6	52	50.0	590	10	Q94JK7
7	51	49.0	291	2	Q9WX38
8	51	49.0	386	16	Q8YRE3
9	50	48.1	125	4	Q9NV61
10	50	48.1	240	4	Q8TCU1
11	49	47.1	2447	5	Q9NEP9
12	49	47.1	4072	5	Q9W4Y4
13	48	46.2	148	2	Q9ZHI4
14	48	46.2	250	5	Q20327
15	47	45.2	97	6	Q9SKT8
16	47	45.2	138	6	Q9TBB8

17	47	45.2	194	11	Q925Q6	Q92566 mesocricetu
18	47	45.2	235	12	P87580	P87580 cydia pomon
19	47	45.2	317	16	Q97HN1	Q97HN1 clostridium
20	47	45.2	375	11	Q99J35	Q99J35 mus musculu
21	47	45.2	870	5	Q96TJ6	Q96TJ6 ancylostoma
22	46	44.2	148	16	Q9KN81	Q9KN81 vibrio chol
23	46	44.2	177	16	Q8U915	Q8U915 agrobacteri
24	46	44.2	966	5	Q22378	Q22378 caenorhabdi
25	45	43.3	350	2	Q9XC99	Q9XC99 mycobacteri
26	45	43.3	388	5	Q17002	Q17002 anopheles g
27	45	43.3	435	11	Q60690	Q60690 mus musculu
28	45	43.3	457	2	Q8RSE1	Q8RSE1 chlorobium
29	45	43.3	530	11	Q8QZ21	Q8QZ21 mus musculu
30	45	43.3	547	4	Q9Y655	Q9Y655 homo sapien
31	45	43.3	576	4	Q9H922	Q9H922 homo sapien
32	45	43.3	620	4	Q9P2K5	Q9P2K5 homo sapien
33	45	43.3	2931	5	Q9W2C6	Q9W2C6 drosophila
34	45	43.3	3389	4	Q960U9	Q960U9 homo sapien
35	45	43.3	3508	4	Q96RM4	Q96RM4 homo sapien
36	44.5	42.8	693	10	Q8S7C8	Q8S7C8 oryza sativ
37	44.5	42.8	735	11	Q9D4G3	Q9D4G3 mus musculu
38	44.5	42.8	735	11	Q9QWJ0	Q9QWJ0 mus musculu
39	44.5	42.8	735	11	Q60718	Q60718 mus musculu
40	44	42.3	137	12	Q914Q8	Q914Q8 hepatitis c
41	44	42.3	137	12	Q914Q7	Q914Q7 hepatitis c
42	44	42.3	137	12	Q914Q6	Q914Q6 hepatitis c
43	44	42.3	137	12	Q914Q5	Q914Q5 hepatitis c
44	44	42.3	137	12	Q914Q4	Q914Q4 hepatitis c
45	44	42.3	137	12	Q914Q3	Q914Q3 hepatitis c

ALIGNMENTS

RESULT 1

Q9BP57 PRELIMINARY: PRT; 61 AA.
AC Q9BP57;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Conotoxin scaffold 1.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilday V., Avidan N., Ben-Asher E., Levy Z.,
FA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL: AF215088; AAC60509.1; -.
DR HSSP: P50985; IAKG.
SQ SEQUENCE 61 AA; 6363 MW; 42E003334D66922 CRC64;

Query Match 95.2%; Score 99; DB 5; Length 61;
Best Local Similarity 93.8%; Pred. No. 5.4e-09;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDYC 16
Db 45 GCCSLPPCALNPDYC 60

RESULT 2

Q9BP56 PRELIMINARY: PRT; 61 AA.
AC Q9BP56;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Conotoxin scaffold I.
 OS Conus pennaceus (Feathered cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 ON NCBI_TaxID=37335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21105969; PubMed=1158371;
 RA Conticello S.G., Glad Y., Avidan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
 RL Mol. Biol. Evol. 18:120-131(2001).
 DR EMBL: AF215089; A060510.1; -.
 DR HSSP: P50985; IAKG.
 SQ SEQUENCE 61 AA; 6348 MW; 6FCFD333D306921 CRC64;
 QY 1 GCCSLPPCALNPDYC 16
 DB 45 GCCSLPPCALNPDYC 60
 QY 027591 PRELIMINARY; PRT; 149 AA.
 ID 027591;
 AC 027591;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE NADP-reducing hydrogenase, subunit A.
 GN MTH1548.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 ON NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vitare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jivani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.,
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 DR EMBL: AE000915; AAB86022.1; -.
 DR InterPro: IPR002023; Cmplx1_24kDa.
 DR Pfam: PF01257; complex1_24kD; 1.
 DR ProDom: PD003859; Cmplx1_24kDa; 1.
 KW Complete proteome.
 SQ SEQUENCE 149 AA; 16433 MW; 351133767604DF9D CRC64;
 QY 1 GCCSLPPCALNPD 14
 DB 118 GCCSLPPCALNPD 131
 QY 095255 PRELIMINARY; PRT; 175 AA.
 ID 095255;
 AC 095255;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative soxR-like transcriptional regulator.
 GN SC01697 OR SC130A.18C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 ON NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Oliver K., Harris D.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redendach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinasli H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Huang C.-H., Kleser I., Jarke L., Murthy J., Hornsby T., Howarth S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: AL096811; CAB6795.1; -.
 DR InterPro: IPR000551; HTH_Merr.
 DR Pfam: PF00376; merr; 1.
 DR PRINTS: PR00040; HTHMERR.
 DR SMART: SM00422; HTH_MERR; 1.
 DR DNA-binding; Transcription regulation.
 SQ SEQUENCE 175 AA; 19358 MW; 27E000CA58867082 CRC64;
 QY 1 GCCSLPPCALNPD 14
 DB 122 GCSLPPCALNPD 135
 QY 045993 PRELIMINARY; PRT; 260 AA.
 ID 045993;
 AC 045993; 062282;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE H02K04.1 protein.
 GN H02K04.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.

```

OX NCB1_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Basham V.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Crixton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Keshaw J., Kirsten J., Laister N., Latreille P.,
RA Lighting J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Smalton N., Smith A., Sonnhammer E., Staden K., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [3]
RP SEQUENCE FROM N.A.
RP White S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: Z81142; CAB03511.1; -. JOINED.
DR EMBL: AL023813; CAB03511.1; -.
DR EMBL: AL023813; CAI9425.1; -.
DR EMBL: Z81142; CAI9425.1; JOINED.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SMO034; CLECT; 1.
DR PROSITE: PSS0041; C_TYPE_LECTIN_2; 1.
SO SEQUENCE 260 AA; 28198 MW; 57E161798F9E604E CRC64;

```

Query Match	50.0%	Score 52;	DB 5;	Length 260;
Best Local Similarity	50.0%;	Pred. No. 1;		
Matches 7; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0;

QY	3	CSLPGCALNPDYC	16
	1	: :	
Db	102	CAAPPCAVTDPYC	115

RESULT 6	
094JK7	
ID	094JK7
AC	094JK7
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	P0434B04.16 protein.
GN	P0434B04.16
OS	Oryza sativa (Rice).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	Eurharicotidae; Oryzeae; Oryza.
OX	NCBI_TaxID=4550;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV. NIPPONBARE;
RA	Sasaki T., Matsumoto T., Yamamoto K.;
RT	"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT	clone:PD434B04."
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
SR	EMBL; AP002540; BAB3995.1; --
SO	SEQUENCE 590 AA; 66477 MW; BCA77D10C9530EB8 CRC64;

Query Match	50.0%;	Score 52;	DB 10;	Length 590;
Best Local Similarity	60.0%;	Pred. No. 2,2;		
Matches	9;	Conservative	2;	Mismatches 4;
				Indels 0;
				Gaps 0;
QY	1	GGCSLPPCALNNPDY	15	

Db 282 GCCTLHSVALNNQNY 296

RESULT 7	
Q9WX38	
ID Q9WX38	PRELIMINARY; PRT; 291 AA

DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ORF291 (Fragment)
DE Anabaena variabilis
OS Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena
NCBI_TaxID=1172;

RN SEQUENCE FROM N.A.
 RP [1]
 RC STRAIN=M3;
 RX MEDLINE=99216503; PubMed=10198437;
 RA Maruyama K., Sato N., Ohta N.;
 RT "Conservation of structure and cold-regulation of RNA-binding proteins
 in cyanobacteria: probable convergent evolution with eukaryotic
 glycine-rich RNA-binding proteins";
 RL Nucleic Acids Res. 27:12029-12036(1999).

FT	NON_TER	291	291
SQ	SEQUENCE	291 AA;	31411 MW; 9D99A032867D49FE CRC64;

Query Match	49.0%;	Score 51;	DB 2;	Length 291;
Best Local Similarity	50.0%;	Pred. No. 1.7;		
Matches	7;	Conservative	4;	Mismatches 3; Indels 0; Gaps 0;

```
QY      3 CSLPPCALNNDYC 16  
      |::||| |: |: |  
Db     108 CAVPPCLLSVPEAC 121
```

RESULT 8
Q8YTE3
ID Q8YTE3
PRELIMINARY;
PRT; 386 AA

DT 01-MAR-2002 (Tremblurel. 20, Created)
DT 01-MAR-2002 (Tremblurel. 20, Last sequence update)
DT 01-MAR-2002 (Tremblurel. 20, Last annotation update)
DE Hypothetical protein A112776.

OS *Anabaena* sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
OX NCBI_TaxID=103690;

RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriduchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yanada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium *Anabaena* sp. strain PCC 7120.";

DR EMBL; AP003590; BAB74475.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 386 AA; 41775 MW; 261618991B197C61 CRC64;

Query Match	49.0%;	Score 51;	DB 16;	Length 386;
Best Local Similarity	50.0%;	Pred. No. 2.2;		
Matches	7;	Conservative	4;	Mismatches 3; Indels 0; Gaps 0

```
QY      3 CSLPPCALNNPDYC 16
          |::||| |::|
Db     108 CAVPPCLLSVPEAC 121
```

```

RESULT 9
Q9NV61 PRELIMINARY; PRT: 125 AA.
AC Q9NV61:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE OVARC1000060 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARIAN CARCINOMA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiroka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuko Y., Kanehori K.;
RT "MDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK011769; BAA91896.1;
SQ SEQUENCE 125 AA; 13504 MW; F2D324918E3A70B1 CRC64;

Query Match 48.1%; Score 50; DB 4; Length 125;
Best Local Similarity 56.2%; Pred. No. 1.1;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDPYC 16
Db 37 GCCALPPALPAGSDIC 52

RESULT 10
Q8TCU1 PRELIMINARY; PRT: 240 AA.
AC Q8TCU1:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Extra-cellular ribonuclease.
GN RNASE6PL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Emilion G., Mungall A.J., Dunham I., Beck S.,
RA Lemuth-Metzinger V., Shelling A.N., Charnock F.M., Ganesan T.S.;
RT "Physical and transcript map of the region between D6S764 and D6S149
RT on chromosome 6q27, the minimal region of allele loss in ovarian
RT cancer.";
RL OncoGene 20:0-0(2001).
DR EMBL: A419867; CAD12032.1;
SQ SEQUENCE 240 AA; 26439 MW; 86BC6ED9E4F2D4A2 CRC64;

Query Match 48.1%; Score 50; DB 4; Length 240;
Best Local Similarity 56.2%; Pred. No. 2;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDPYC 16
Db 134 GCCALPPALPAGSDIC 149

RESULT 11
Q9NEP9 PRELIMINARY; PRT: 2447 AA.
AC Q9NEP9:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

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DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EG:BACR2583.1 protein.
GN EG:BACR2583.1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy L., Harris D., Barrell B.;
RT "Sequencing the distal X chromosome of Drosophila melanogaster.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Benos P.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL138972; CAB72286.1;
DR HSSP: Q07954; 1CR8.
DR FLYBase: FBgn0040381; EG:BACR25B3.1.
DR InterPro: IPR001525; C5_DNA_meth.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003598; 19_c2.
DR InterPro: IPR003006; 19_MHC.
DR InterPro: IPR000034; Laminin_B.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR002172; LDL_receptl_A.
DR Pfam: P00047; 19; 2.
DR Pfam: P00052; Laminin_B; 3.
DR Pfam: P00053; Laminin_EGF; 4.
DR Pfam: P00057; ldl_receptl_a; 23.
DR PRINTS: PR00011; EGF_LAMININ.
DR PRINTS: PR00261; LDLRECEPTOR.
DR ProDom: PD003031; Laminin_B; 3.
DR SMART: SM00180; EGF_Lam; 2.
DR SMART: SM00001; EGF-like; 3.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00281; Lamb; 3.
DR SMART: SM00192; LDLA; 23.
DR PROSITE: PS00094; C5_MTASE_1; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_7.
DR PROSITE: PS01186; EGF_2; 4.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; 7.
DR PROSITE: PS01209; LDLRA_1; 20.
DR PROSITE: PS00068; LDLRA_2; 23.
DR EGF-like domain; Glycoprotein; Immunoglobulin domain;
KW Laminin EGF-like domain; Repeat.
SQ SEQUENCE 2447 AA; 270120 MW; 3DAE695C54090ED4 CRC64;

Query Match 47.1%; Score 49; DB 5; Length 2447;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCCSLPPCALNPDPYC 16
Db 2406 GSCSLPCDVSNTESC 2421

RESULT 12
Q9W4Y4 PRELIMINARY; PRT: 4072 AA.
AC Q9W4Y4:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Pcan protein.
GN PCAN OR EG:BACR25B3.11 OR CG7981.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

```


RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Cocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
 RA Abil J.F., Ayabayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotler J.,
 RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
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 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck C.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Klamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei I., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.R., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Slen T.,
 RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003424; AAF45786.2; -;
 DR HSSP: P00740; 1PDM.
 DR FLYBase; FBgn0027946; pcan.
 DR InterPro: IPR001525; C5_DNA_meth.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003600; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR000034; Laminin_B.
 DR InterPro: IPR002049; Laminin_G.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR002172; LDL_recept_A.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF00047; Ig_12.
 DR Pfam: PF00052; laminin_B; 3.
 DR Pfam: PF00053; laminin_EGF; 4.
 DR Pfam: PF00054; laminin_G; 3.
 DR Pfam: PF00057; ldl_recept_a; 23.
 DR PRINTS: PR00261; LDLRECEPTOR.
 DR PRODOM: PD003031; Laminin_B; 3.
 DR SMART: SM00180; EGF_Lam; 2.
 DR SMART: SM00001; EGF_Like; 5.
 DR SMART: SM00408; IGC2; 7.
 DR SMART: SM00410; IG_Like; 4.
 DR SMART: SM00281; Lamb; 3.
 DR SMART: SM00282; Lamb; 3.
 DR SMART: SM00192; LDla; 23.
 DR PROSITE: PS00094; C5_MTASE_1; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_10.
 DR PROSITE: PS01186; EGF_2; 6.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; 7.

DR PROSITE: PS01209; LDLRA_1; 20.
 DR PROSITE: PS50068; LDLRA_2; 23.
 DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
 KW EGF-like domain; Glycoprotein; Immunoglobulin domain;
 KW Laminin EGF-like domain; Repeat.
 SQ SEQUENCE 4072 AA; 449813 MW; 7AE8AA54B5C0A19B CRC64;
 QY 1 GCCSLPPCALNPDYC 16
 DB 2246 GSCSLPCPDVSNESC 2261
 RESULT 13
 ID 092HT4 PRELIMINARY; PRT; 148 AA.
 AC 092HT4;
 DT 01-MAY-1999 (TRMBLrel. 10, Created)
 DT 01-MAY-1999 (TRMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
 DE SoxR homolog.
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae.
 OC Chromobacterium.
 NCBI_TaxID=536;
 RN 11)
 RP SEQUENCE FROM N.A.
 RA Kolbachuk D.J., Dennis D.E.;
 RT "Chromobacterium violaceum genomic fragment containing orfD (soxR/merR homolog)";
 RT homology";
 RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.
 CC 1- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: AF061445; AAC69613.1; -;
 DR InterPro: IPR000551; HTH_Merr.
 DR Pfam: PF00376; merr; 1.
 DR PRINTS: PR00040; HTHMERR.
 DR SMART: SM00422; HTH_MERR; 1.
 DR PROSITE: PS00552; HTH_MERR_FAMILY; 1.
 DR DNA-binding; Transcription regulation.
 SQ SEQUENCE 148 AA; 16441 MW; 16805040BA7C0827 CRC64;
 Query Match 46.2%; Score 48; DB 2; Length 148;
 Best Local Similarity 64.3%; Pred. No. 2.8;
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 GCCSLPPCALNPD 14
 DB 117 GCSLSECKLYNPD 130
 RESULT 14
 ID 020327 PRELIMINARY; PRT; 250 AA.
 AC 020327;
 DT 01-NOV-1996 (TRMBLrel. 01, Created)
 DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TRMBLrel. 20, Last annotation update)
 DE Hypothetical 27.7 kDa protein.
 GN F42C5.7.
 GN Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodertinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN 11)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE-99069613; PubMed-9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for

RT Investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Du Z.;
 RT "The sequence of C. elegans cosmid F42C5";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U40799; AA81484.1;
 DR InterPro; IPR001467; PROK_Mboxred.
 DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 250 AA; 27685 MW; 477A9EC12E3C3585 CRC64;

Query Match 46.2%; Score 48; DB 5; Length 250;
 Best Local Similarity 50.0%; Pred. No. 4.5;
 Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

OY 1 GCCSL--PPCALNNPDYC 16
 ||||| ||| |.
 DB 61 GCCSMGPPCPPPPPMC 78

RESULT 15

ID 095KL8 PRELIMINARY; PRT; 97 AA.
 AC 095KL8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE Tissue inhibitor of matrix metalloproteinase-2 (Fragment).
 GN TIMP-2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA Ji S., Wang Y., Li H., Ji W., Piao Y.;
 RT "Cloning and characterization of tissue inhibitor of matrix
 metalloproteinase-2 (TIMP-2) cDNA from Macaca mulatta."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF366398; AAK53705.1;
 DR InterPro; IPR001820; TIMP.
 DR Pfam; PF00965; TIMP; 1.
 FT NON_TER 1
 SQ SEQUENCE 97 AA; 11224 MW; 1AA2387A2802533C CRC64;

Query Match 45.2%; Score 47; DB 6; Length 97;
 Best Local Similarity 36.4%; Pred. No. 2.8;
 Matches 8; Conservative 4; Mismatches 4; Indels 6; Gaps 1;

OY 1 GC-----CSLPPCALNNPDYC 16
 || | : ||::|| |
 DB 28 GCCKITRCPIPCYISSPDEC 49

Search completed: January 8, 2003, 15:29:57
 Job time : 26.7576 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 15:24:04 ; Search time 31.9394 Seconds
(without alignments)
70.924 Million cell updates/sec

Title: US-09-897-465-1

Perfect score: 55

Sequence: 1 XXCCXXPCXXXXXXC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	69.1	42	21	AA21603
2	37	67.3	16	20	AA24157
3	37	67.3	16	20	AA24157
4	36	65.5	16	20	AA24160
5	36	65.5	16	20	AA24162
6	36	65.5	16	20	AA24162
7	36	65.5	16	20	AA24162
8	36	65.5	16	20	AA24162
9	36	65.5	16	20	AA24162
10	36	65.5	16	20	AA24162

11	36	65.5	40	21	AA21591	Cone snail alpha-c
12	36	65.5	40	21	AA21597	Cone snail alpha-c
13	36	65.5	40	21	AA21624	Cone snail alpha-c
14	36	65.5	56	21	AA21427	Cone snail alpha-c
15	36	65.5	62	21	AA21616	Cone snail alpha-c
16	35	63.6	16	16	AA21527	A-lineage conotoxin
17	35	63.6	16	16	AA21527	A-lineage conotoxin
18	35	63.6	16	16	AA21527	A-lineage conotoxin
19	35	63.6	16	16	AA21527	A-lineage conotoxin
20	35	63.6	16	16	AA21527	A-lineage conotoxin
21	35	63.6	16	16	AA21527	A-lineage conotoxin
22	35	63.6	16	16	AA21527	A-lineage conotoxin
23	35	63.6	16	16	AA21527	A-lineage conotoxin
24	35	63.6	16	16	AA21527	A-lineage conotoxin
25	35	63.6	16	16	AA21527	A-lineage conotoxin
26	35	63.6	16	16	AA21527	A-lineage conotoxin
27	35	63.6	16	16	AA21527	A-lineage conotoxin
28	35	63.6	16	16	AA21527	A-lineage conotoxin
29	35	63.6	16	16	AA21527	A-lineage conotoxin
30	35	63.6	16	16	AA21527	A-lineage conotoxin
31	35	63.6	16	16	AA21527	A-lineage conotoxin
32	35	63.6	16	16	AA21527	A-lineage conotoxin
33	35	63.6	16	16	AA21527	A-lineage conotoxin
34	35	63.6	16	16	AA21527	A-lineage conotoxin
35	35	63.6	16	16	AA21527	A-lineage conotoxin
36	35	63.6	16	16	AA21527	A-lineage conotoxin
37	35	63.6	16	16	AA21527	A-lineage conotoxin
38	35	63.6	16	16	AA21527	A-lineage conotoxin
39	35	63.6	16	16	AA21527	A-lineage conotoxin
40	35	63.6	16	16	AA21527	A-lineage conotoxin
41	35	63.6	16	16	AA21527	A-lineage conotoxin
42	35	63.6	16	16	AA21527	A-lineage conotoxin
43	35	63.6	16	16	AA21527	A-lineage conotoxin
44	35	63.6	16	16	AA21527	A-lineage conotoxin
45	35	63.6	16	16	AA21527	A-lineage conotoxin

ALIGNMENTS

RESULT 1
ID AAB21603 standard; Peptide: 42 AA.
XX AAB21603;
AC AAB21603;
XX 19-JAN-2001 (first entry)
XX Cone snail alpha-conotoxin SEQ ID NO: 334.
DE Cone snail alpha-conotoxin; venom; disulphide bond; mood disorder;
KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
KW gastric motility disorder; urinary incontinence; nicotine addiction;
KW small cell lung carcinoma.
XX Conus lividus.
PN WO200044776-A1.
XX 03-AUG-2000.
PD 28-JAN-2000; 2000MO-US01979.
XX 29-JAN-1999; 99US-0118381.
PR (UTAH) UNIV UTAH RES FOUND.
PA (COGN-) COGNEX INC.
XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;
XX WPI; 2000-505965/45.
XX N-PSDB; AAA89499.

PT alpha-conotoxin polypeptides derived from the venom of cone snails
 PT useful e.g. as neuromuscular blocking agents for use in surgery and for
 PT treating unipolar depression -
 PS
 PS Claim 39; Page 58; 229pp; English.
 CC The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The
 CC alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
 CC and for treating disorders regulated at the neuronal nicotinic
 CC acetylcholine receptors, including cardiovascular disorders, gastric
 CC motility disorders, urinary incontinence, nicotine addiction, mood
 CC disorders such as bipolar disorder, unipolar depression, dysthymia and
 CC seasonal affective disorder, and small cell lung carcinoma.
 CC
 SQ Sequence 42 AA;
 QY
 DB 3 CCXXPCXKXXXXXC 17
 DB 24 CSHPCACGSMHIC 38
 Query Match 69.1%; Score 38; DB 21; Length 42;
 Best Local Similarity 33.3%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 RESULT 2
 ID AAY24157 standard; peptide; 16 AA.
 AC AAY24157;
 DT 10-SEP-1999 (first entry)
 DE Alpha-conotoxin peptide SEQ ID NO:4.
 XX
 KW Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;
 KW small cell lung carcinoma; cardiovascular disorder; nicotine addiction;
 KW gastric motility disorder; urinary incontinence; mood disorder;
 KW bipolar disorder; unipolar depression; dysthymia;
 KW seasonal effective disorder.
 XX
 OS Conus magus.
 OS Synthetic.
 XX
 PN WO933482-A1.
 XX
 PD 08-JUL-1999.
 XX
 PF 23-DEC-1998; 98WO-US27367.
 XX
 PR 03-APR-1998; 98US-0080588.
 PR 31-DEC-1997; 97US-0070153.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Cartier GE, Luo S, McIntosh JM, Olivera BM, Yoshikami D;
 XX
 DR WPI; 1999-405367/34.
 XX
 PT Alpha-conotoxin peptides that are used to treat disorders regulated
 PT at neuronal nicotinic acetylcholine receptors
 PS
 PS Claim 12; Page 27; 40pp; English.
 CC The present sequence represents a specifically claimed example of an
 CC alpha-conotoxin from the general formula given in AAY24157, which can be
 CC used to treat disorders regulated at neuronal nicotinic acetylcholine
 CC receptors (nAChR). The alpha-conotoxins are useful for preparing a

CC pharmaceutical composition for treating disorders regulated at neuronal
 CC nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing
 CC nAChR. Disorders that can be treated include cardiovascular disorders, a
 CC gastric motility disorder, urinary incontinence, nicotine addiction, a
 CC mood disorder or small cell lung carcinoma. Mood disorders include
 CC bipolar disorder, unipolar depression, dysthymia and seasonal effective
 CC disorder. The alpha-conotoxins can also be used for diagnosis of small
 CC cell lung carcinoma. The alpha-conotoxin antagonists are able to
 CC discriminate between non-symmetrical ligand binding interfaces present
 CC on the nAChR. The alpha-conotoxin has the ability to potentially block any
 CC receptor containing a alpha beta subunit interface, regardless of what
 CC other subunits may be present in the receptor complex.
 CC
 SQ Sequence 16 AA;
 QY
 DB 3 CCXXPCXKXXXXXC 17
 DB 2 CCNPFVCFATHSMLC 16
 Query Match 67.3%; Score 37; DB 20; Length 16;
 Best Local Similarity 33.3%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 RESULT 3
 ID AAY09521 standard; peptide; 16 AA.
 AC AAY09521;
 DT 20-JUL-1999 (first entry)
 DE Alpha conopeptide MII chimera SEQ ID NO:3.
 XX
 KW Alpha conopeptide MII; alpha-4/7 conotoxin; cardiovascular agent;
 KW neuronal nicotinic acetylcholine receptor; small cell lung carcinoma;
 KW detection; gastric motility; urinary incontinence; anti-smoking agent.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 2..8
 FT Disulfide-bond 3..16
 XX
 PN WO9921878-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 23-OCT-1998; 98WO-US22368.
 XX
 PR 14-NOV-1997; 97US-0065814.
 PR 24-OCT-1997; 97US-0062783.
 XX
 PA (COGN-) COGNETIX INC.
 PA (SALK) SALK INST.
 PA (UYCA-) UNIV CASE WESTERN RESERVE.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Cartier GE, Koerber SC, McIntosh JM, Olivera BM;
 PI Rivier JE, Shen GS, Shonk, Yoshikami D;
 XX
 DR WPI; 1999-326687/27.
 XX
 PT Derivatives of alpha-conotoxin and their analogues
 PS
 PS Example 11; Page 51; 176pp; English.
 CC The present invention describes derivatives (I) of alpha-conotoxin MII
 CC (II), an alpha-4/7 conotoxin peptide, with practically the same activity
 CC as (II). (I), and its mimetics, are useful as cardiovascular agents;
 CC for treating or diagnosing small-cell lung carcinoma; and as gastric
 CC motility, urinary incontinence and anti-smoking agents. (I) and their
 CC mimetics can be designed to be selective for particular subtypes of

CC neuronal nicotinic acetylcholine receptor, particularly the alpha 3 beta
CC 2 and alpha 3 beta 4 subtypes. The present sequence represents a
CC peptide from an example from the present invention.
XX

Sequence 16 AA;

Query Match	67.3%	Score 37;	DB 20;	Length 16;
Best Local Similarity	33.3%;	Pred. No. 51;		
Matches	5;	Conservative	0;	Mismatches 10;
			Indels	0;
			Gaps	0;

QY	3	CCXXPXCCCCXXC	17
	11	11	
Db	2	CCSNPVCFATNSLC	16

RESULT 4
AAY24160
ID AAY24160 standard; peptide; 16 AA
VY

AC	AAV24160;
XX	
DT	10-SEP-1999 (first entry)
XX	

DE xy	Alpha-conotoxin peptide SEQ ID NO:5.

KM Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;
KM small cell lung carcinoma; cardiovascular disorder; nicotine addiction
KM gastric motility disorder; urinary incontinence; mood disorder;
KM bipolar disorder; unipolar depression; dysthymia;
KM seasonal affective disorder.

05 *Conus aulicus*.

PN W09933482-A1.

PD 08-JUL-1999.

PF 23-DEC-1998; 98WO-US27367.

PR	03-APR-1998;	98US-0080588.
PR	03-APR-1998;	98US-0080588.
PR	03-APR-1998;	98US-0080588.

31-DEC-1997; 97US-0070153.

PA (UTAH) UNIV UTAH RES FOUND.
XX

PI Cartier GE, Luo S, McIntosh JM, Olivera BM, Yoshikami D;
xy

DR WPI; 1999-405367/34.

PT Alpha-conotoxin peptides that are used to treat disorders regulated
PT at neuronal nicotinic acetylcholine receptors
PT

Claim 28; Page 6; 40pp; English.

The present sequence represents a specifically claimed example of an alpha-conotoxin, which can be used to treat disorders regulated at neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins are useful for preparing a pharmaceutical composition for treating disorders regulated at neuronal nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be treated include cardiovascular disorders, a gastric motility disorder, urinary incontinence, nicotine addiction, a mood disorder or small cell lung carcinoma. Mood disorders include bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder. The alpha-conotoxins can also be used for diagnosis of small cell lung carcinoma. The alpha-conotoxin antagonists are able to discriminate between non-symmetrical ligand binding interfaces present on the nAChR. The alpha-conotoxin has the ability to potentially block any receptor containing a alpha beta subunit interface, regardless of what other subunits may be present in the receptor complex.

SQ Sequence 16 AA;

Query Match	65.58;	Score 36;	DB 20;	Length 16;
-------------	--------	-----------	--------	------------

Best Local	Similarity	33.38;	Pred. No.	70;
Matches	5; Conservative	0;	Mismatches	10; Indels
				0; Gaps

Qy	3	CCXXPXCCCCXXXC	17
Db	2	CCSYPCFATNSDYC	16

```

RESULT 5
AAY24162
ID AAY24162 standard; peptide; 16 AA
XY

```

AC AAY24162;
xy

DT 10-SEP-1999 (first entry)
 YY

DE XY	Alpha-conotoxin peptide SEQ ID NO:8

KM seasonal affective disorder.
KM bipolar disorder; unipolar depression; dysthymia;
KM seasonal effective disorder.
KM gastric motility disorder; urinary incontinence; mood disorder;
KM small cell lung carcinoma; cardiovascular disorder; nicotine addiction;
KM alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;
KM Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;

05 Conus aulicus.
yx

PN WO9933482-A1.
YY

PD 08-JUL-1999
XY

PE 23-DEC-1998; 98WO-US27367.
XX

PR	03-APR-1998;	98US-0080588.
PR	31-DEC-1997.	97US-0070153

XX
PA (TITAH) INTY TTAH REC FOUND

XX	Carrier GF	fino e	Mattoc
PI			

XX
DB WPT: 1999-405367/34

PT	Alpha-conotoxin pent
XX	
XX	

Claim 28. Para 6. Above. English
XX al neuronal nicotinic acetylcholine receptors

The present sequence represents

The present sequence represents a specifically claimed example of an alpha-conotoxin, which can be used to treat disorders regulated at neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins are useful for preparing a pharmaceutical composition for treating disorders regulated at neuronal nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be treated include cardiovascular disorders, a gastric motility disorder, urinary incontinence, nicotine addiction, a mood disorder or small cell lung carcinoma. Mood disorders include bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder. The alpha-conotoxins can also be used for diagnosis of small cell lung carcinoma. The alpha-conotoxin antagonists are able to discriminate between non-symmetrical ligand binding interfaces present on the nAChR. The alpha-conotoxin has the ability to potentially block any receptor containing a alpha beta subunit interface, regardless of what other subunits may be present in the receptor complex.

Sequence	16 AA;
50	

Query Match	65.5%;	Score 36;	DB 20;	Length 16;
Best Local Similarity	33.3%;	Pred. No. 70;		
Matches	5;	Conservative	0;	Mismatches 10;
			Indels	0;
			Gaps	0;

QY	3	CCXXPCXXXXXXXXC	17
Db	2	CCSYPCFATNSGYC	16

RESULT 6

ID AAY09524 standard; peptide; 16 AA.

XX AAY09524;

DT 20-JUL-1999 (first entry)

DE Alpha conotoxin peptide SEQ ID NO:6.

XX Alpha conopeptide MII; alpha-4/7 conotoxin; cardiovascular agent;

KM neuronal nicotinic acetylcholine receptor; small cell lung carcinoma;

XX detection; gastric motility; urinary incontinence; anti-smoking agent.

XX Conus aulicus.

XX WO9921878-A1.

XX 06-MAY-1999.

XX 23-OCT-1998; 98WO-US22368.

XX 14-NOV-1997; 97US-0065814.

XX 24-OCT-1997; 97US-0062783.

XX (COGN-) COGNEX INC.

XX (SALK) SALK INST.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX (UTAH) UNIV UTAH RES FOUND.

XX Cartier GE, Koerber SC, McIntosh JM, Olivera BM;

XX Rivier JE, Shen GS, Shonk, Yoshikami D;

XX WPI; 1999-326687/27.

XX Derivatives of alpha-conotoxin and their analogues

XX Example 11; Page 51; 176pp; English.

XX The present invention describes derivatives (I) of alpha-conotoxin MII

XX as (II), an alpha-4/7 conotoxin peptide, with practically the same activity

XX for treating or diagnosing small-cell lung carcinoma; and as gastric

XX motility, urinary incontinence and anti-smoking agents. (I) and their

XX mimetics can be designed to be selective for particular subtypes of

XX neuronal nicotinic acetylcholine receptor, particularly the alpha 3 beta

XX 2 and alpha 3 beta 4 subtypes. The present sequence represents a

XX peptide from an example from the present invention.

XX Sequence 16 AA;

XX Query Match 65.5%; Score 36; DB 20; Length 16;

XX Best Local Similarity 33.3%; Pred. No. 70;

XX Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

XX 3 CCXXPCXKXXXXXXC 17

XX 2 CCXXPCXKXXXXXXC 16

XX Db

XX RESULT 7

XX AAW89493

XX ID AAW89493 standard; Protein; 16 AA.

XX AAW89493;

XX 12-MAR-1999 (first entry)

XX Conopeptide AuiA.

XX Conopeptide: Conus aulicus; AuiA; AuiB; AuiC; nAChR; neurotransmitter;

XX neuronal nicotinic acetylcholine receptor; presynaptic release;

KM tobacco addiction; cardiovascular; gastric motility disorder;

KM urinary incontinence.

XX Conus aulicus.

XX Key Location/Qualifiers

XX Disulfide-bond 2..8

XX Disulfide-bond 3..16

XX WO9851322-A1.

XX 19-NOV-1998.

XX 09-APR-1998; 98WO-US07004.

XX 15-MAY-1997; 97US-0857068.

XX (UTAH) UNIV UTAH RES FOUND.

XX Cartier GE, Luo S, McIntosh JM, Olivera BM, Yoshikami D;

XX WPI; 1999-059683/05.

XX Claim 10; Page 19; 22pp; English.

XX The present sequence represents a specifically claimed conopeptide.

XX Conopeptides are used to target neuronal nicotinic acetylcholine

XX receptors (nAChRs) and selectively modulate the presynaptic release

XX of specific neurotransmitters, for example in the treatment of tobacco

XX addiction, cardiovascular and gastric motility disorders, and urinary

XX incontinence.

XX Sequence 16 AA;

XX Query Match 65.5%; Score 36; DB 20; Length 16;

XX Best Local Similarity 33.3%; Pred. No. 70;

XX Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

XX 3 CCXXPCXKXXXXXXC 17

XX 2 CCXXPCXKXXXXXXC 16

XX Db

XX RESULT 8

XX AAW89495

XX ID AAW89495 standard; Protein; 16 AA.

XX AAW89495;

XX 12-MAR-1999 (first entry)

XX Conopeptide AuiC.

XX Conopeptide: Conus aulicus; AuiA; AuiB; AuiC; nAChR; neurotransmitter;

XX neuronal nicotinic acetylcholine receptor; presynaptic release;

XX tobacco addiction; cardiovascular; gastric motility disorder;

XX urinary incontinence.

XX Conus aulicus.

XX Key Location/Qualifiers

XX Disulfide-bond 2..8

XX Disulfide-bond 3..16

XX WO9851322-A1.

XX 19-NOV-1998.

XX 09-APR-1998; 98WO-US07004.

PR 15-MAY-1997; 97US-0857068.
 XX (UTAH) UNIV UTAH RES FOUND.
 PA
 PI Cartier GE, Luo S, McIntosh JM, Olivera BM, Yoshikami D;
 XX WPI: 1999-059683/05.
 DR
 XX New conopeptides AuiA, AuiB, and AuiC - target neuronal nicotinic
 PT acetylcholine receptors and modulate neurotransmitter release
 PI
 XX Claim 12; Page 19; 22pp; English.
 PS
 CC The present sequence represents a specifically claimed conopeptide.
 CC Conopeptides are used to target neuronal nicotinic acetylcholine
 CC receptors (nAChRs) and selectively modulate the presynaptic release
 CC of specific neurotransmitters, for example in the treatment of tobacco
 CC addiction, cardiovascular and gastric mobility disorders, and urinary
 CC incontinence.
 CC
 SO Sequence 16 AA;
 XX

Query Match 65.5%; Score 36; DB 20; Length 16;
 Best Local Similarity 33.3%; Pred. No. 70;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPCFATNSGYC 17
 II I I
 Db 2 CCSTPCFATNSGYC 16

RESULT 9
 AAY24166
 ID AAY24166 standard; peptide: 17 AA.
 XX

AC AAY24166;

DT 10-SEP-1999 (first entry)

DE Alpha-conotoxin peptide SEQ ID NO:6.

XX Alpha-conotoxin: neuronal nicotinic acetylcholine receptor; nAChR;
 KW small cell lung carcinoma; cardiovascular disorder; nicotine addiction;
 KW gastric motility disorder; urinary incontinence; mood disorder;
 KW bipolar disorder; unipolar depression; dysthymia;
 KW seasonal affective disorder.
 XX

OS Conus aulicus.

OS Synthetic.

PN WO9933482-A1.

PD 08-JUL-1999.

PF 23-DEC-1998; 98WO-US27367.

PR 03-APR-1998; 98US-0080588.

PR 31-DEC-1997; 97US-0070153.

XX (UTAH) UNIV UTAH RES FOUND.

PI Cartier GE, Luo S, McIntosh JM, Olivera BM, Yoshikami D;
 WPI: 1999-405367/34.

DR

XX Alpha-conotoxin peptides that are used to treat disorders regulated
 PT at neuronal nicotinic acetylcholine receptors
 XX

PS Disclosure; Page 6; 40pp; English.

CC The present sequence represents an example of an alpha-conotoxin
 CC peptide from the general formula given in AAY24155, which can be
 CC used to treat disorders regulated at neuronal nicotinic acetylcholine

CC receptors (nAChR). The alpha-conotoxins are useful for preparing a
 CC pharmaceutical composition for treating disorders regulated at neuronal
 CC nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing
 CC nAChR. Disorders that can be treated include cardiovascular disorders, a
 CC gastric motility disorder, urinary incontinence, nicotine addiction, a
 CC mood disorder or small cell lung carcinoma. Mood disorders include
 CC bipolar disorder, unipolar depression, dysthymia and seasonal affective
 CC disorder. The alpha-conotoxins can also be used for diagnosis of small
 CC cell lung carcinoma. The alpha-conotoxin antagonists are able to
 CC discriminate between non-symmetrical ligand binding interfaces present
 CC on the nAChR. The alpha-conotoxin has the ability to potentially block any
 CC receptor containing an alpha beta subunit interface, regardless of what
 CC other subunits may be present in the receptor complex.
 CC
 SO Sequence 17 AA;
 XX

Query Match 65.5%; Score 36; DB 20; Length 17;
 Best Local Similarity 33.3%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPCFATNSGYC 17
 II I I
 Db 3 CCSTPCFATNSGYC 17

RESULT 10
 AAB21590
 ID AAB21590 standard; Peptide: 39 AA.
 XX

AC AAB21590;

DT 19-JAN-2001 (first entry)

DE Cone snail alpha-conotoxin SEQ ID NO: 308.

XX Cone snail: alpha-conotoxin; venom; disulphide bond; mood disorder;
 KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.
 XX

OS Conus betulinus.

PN WO200044776-A1.

PD 03-AUG-2000.

PF 28-JAN-2000; 2000WO-US01979.

PR 29-JAN-1999; 99US-0118381.

PA (UTAH) UNIV UTAH RES FOUND.
 (COGN-) COGNETIX INC.

PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;
 WPI: 2000-505965/45.

DR N-PSDB: AAA89486.

XX alpha-conotoxin polypeptides derived from the venom of cone snails
 PT useful e.g. as neuromuscular blocking agents for use in surgery and for
 PT treating unipolar depression -
 XX

PS Claim 39; Page 55; 229pp; English.

CC The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The
 CC alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
 CC and for treating disorders regulated at the neuronal nicotinic
 CC acetylcholine receptors, including cardiovascular disorders, gastric

CC motility disorders, urinary incontinence, nicotine addiction, mood
CC disorders such as bipolar disorder, unipolar depression, dysthymia and
CC seasonal affective disorder, and small cell lung carcinoma.
XX

Sequence 39 AA:

Query Match 65.5%; Score 36; DB 21; Length 39;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPCXXXXXXC 17
DB 24 CSHPCSVTHPELC 38

RESULT 11
AAB21591
ID AAB21591 standard; Peptide: 40 AA.

AC AAB21591;

DT 19-JAN-2001 (first entry)

DE Cone snail alpha-conotoxin SEQ ID NO: 310.

KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
KW gastric motility disorder; urinary incontinence; nicotine addiction;
KW small cell lung carcinoma.

XX Conus betulinus.

PN MO200044776-A1.

PD 03-AUG-2000.

PF 28-JAN-2000; 2000WO-US01979.

PR 29-JAN-1999; 99US-0118381.

PA (UTAH) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

DR WPI: 2000-505965/45.

DR N-PSDB; AAA89487.

PT alpha-conotoxin polypeptides derived from the venom of cone snails
PT useful e.g. as neuromuscular blocking agents for use in surgery and for
PT treating unipolar depression -

PS Claim 39; Page 55; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and
XX their coding sequences from a number of different species of cone snail.
XX These peptides are found in minute quantities in the venom of the snails,
XX and are targeted at the neuronal nicotinic acetylcholine receptors of the
XX nervous system. They usually contain two disulphide bonds, which give
XX them defined conformations, a rarity in molecules this small. The
XX alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
XX and for treating disorders regulated at the neuronal nicotinic
XX acetylcholine receptors, including cardiovascular disorders, gastric
XX motility disorders, urinary incontinence, nicotine addiction, mood
XX disorders such as bipolar disorder, unipolar depression, dysthymia and
XX seasonal affective disorder, and small cell lung carcinoma.

XX Sequence 40 AA:

Query Match 65.5%; Score 36; DB 21; Length 40;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
DB 22 CSHPCSVTHPELC 36

RESULT 12
AAB21597
ID AAB21597 standard; Peptide: 40 AA.

AC AAB21597;

DT 19-JAN-2001 (first entry)

DE Cone snail alpha-conotoxin SEQ ID NO: 322.

KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
KW gastric motility disorder; urinary incontinence; nicotine addiction;
KW small cell lung carcinoma.

XX Conus geographus.

PN MO200044776-A1.

PD 03-AUG-2000.

PF 28-JAN-2000; 2000WO-US01979.

PR 29-JAN-1999; 99US-0118381.

PA (UTAH) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

DR WPI: 2000-505965/45.

DR N-PSDB; AAA89493.

PT alpha-conotoxin polypeptides derived from the venom of cone snails
PT useful e.g. as neuromuscular blocking agents for use in surgery and for
PT treating unipolar depression -

PS Claim 39; Page 56; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and
XX their coding sequences from a number of different species of cone snail.
XX These peptides are found in minute quantities in the venom of the snails,
XX and are targeted at the neuronal nicotinic acetylcholine receptors of the
XX nervous system. They usually contain two disulphide bonds, which give
XX them defined conformations, a rarity in molecules this small. The
XX alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
XX and for treating disorders regulated at the neuronal nicotinic
XX acetylcholine receptors, including cardiovascular disorders, gastric
XX motility disorders, urinary incontinence, nicotine addiction, mood
XX disorders such as bipolar disorder, unipolar depression, dysthymia and
XX seasonal affective disorder, and small cell lung carcinoma.

XX Sequence 40 AA:

Query Match 65.5%; Score 36; DB 21; Length 40;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
DB 22 CSHPCAGNNOHC 36

RESULT 13
AAB21624
ID AAB21624 standard; Peptide: 40 AA.

AC AAB21624;

XX 19-JAN-2001 (first entry)
 DT Cone snail alpha-conotoxin SEQ ID NO: 376.
 XX
 DE Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 XX neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.
 XX
 OS Conus purpurascens.
 XX
 PN WO200044776-A1.
 XX
 PD 03-AUG-2000.
 XX
 PE 28-JAN-2000; 2000WO-US01979.
 XX
 PR 29-JAN-1999; 99US-0118381.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX (COGN-) COGNETIX INC.
 XX
 PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;
 XX
 DR WPI; 2000-505965/45.
 DR N-PSDB; AAA89520.
 XX
 PT alpha-conotoxin polypeptides derived from the venom of cone snails
 PT useful e.g. as neuromuscular blocking agents for use in surgery and for
 PT treating unipolar depression -
 XX
 PS Claim 39; Page 63; 229pp; English.
 XX
 CC The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The
 CC alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
 CC and for treating disorders regulated at the neuronal nicotinic
 CC acetylcholine receptors, including cardiovascular disorders, gastric
 CC motility disorders, urinary incontinence, nicotine addiction, mood
 CC disorders such as bipolar disorder, unipolar depression, dysthymia and
 CC seasonal affective disorder, and small cell lung carcinoma.
 XX
 SQ Sequence 40 AA;
 QY 3 CCXXPXCXXXXXC 17
 DB 20 CCSDPSCWRHSLAC 34
 AAB21427
 ID AAB21427 standard; Protein; 56 AA.
 XX
 AC AAB21427;
 XX
 DT 19-JAN-2001 (first entry)
 XX
 DE Cone snail alpha-conotoxin SEQ ID NO: 61.
 XX
 KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.
 XX

OS Conus aulicus.
 XX
 PN WO200044776-A1.
 XX
 PD 03-AUG-2000.
 XX
 PE 28-JAN-2000; 2000WO-US01979.
 XX
 PR 29-JAN-1999; 99US-0118381.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX (COGN-) COGNETIX INC.
 XX
 PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;
 XX
 DR WPI; 2000-505965/45.
 DR N-PSDB; AAA89402.
 XX
 PT alpha-conotoxin polypeptides derived from the venom of cone snails
 PT useful e.g. as neuromuscular blocking agents for use in surgery and for
 PT treating unipolar depression -
 XX
 PS Claim 39; Page 32; 229pp; English.
 XX
 CC The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The
 CC alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
 CC and for treating disorders regulated at the neuronal nicotinic
 CC acetylcholine receptors, including cardiovascular disorders, gastric
 CC motility disorders, urinary incontinence, nicotine addiction, mood
 CC disorders such as bipolar disorder, unipolar depression, dysthymia and
 CC seasonal affective disorder, and small cell lung carcinoma.
 XX
 SQ Sequence 56 AA;
 QY 3 CCXXPXCXXXXXC 17
 DB 41 CCSPPCFATNSDYC 55
 AAB21616
 ID AAB21616 standard; Peptide; 62 AA.
 XX
 AC AAB21616;
 XX
 DT 19-JAN-2001 (first entry)
 XX
 DE Cone snail alpha-conotoxin SEQ ID NO: 360.
 XX
 KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.
 XX
 OS Conus obscurus.
 XX
 PN WO200044776-A1.
 XX
 PD 03-AUG-2000.
 XX
 PE 28-JAN-2000; 2000WO-US01979.
 XX
 PR 29-JAN-1999; 99US-0118381.
 XX

PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.

XX
 PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX
 DR WPI: 2000-505965/45.
 DR N-PSDB; AAA89512.

XX
 PT alpha-conotoxin polypeptides derived from the venom of cone snails
 PT useful e.g. as neuromuscular blocking agents for use in surgery and for
 PT treating unipolar depression

PS Claim 39: Page 61; 229pp: English.

XX
 CC The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The
 CC alpha-conotoxins can be used as neuromuscular blocking agents in surgery,
 CC and for treating disorders regulated at the neuronal nicotinic
 CC acetylcholine receptors, including cardiovascular disorders, gastric
 CC motility disorders, urinary incontinence, nicotine addiction, mood
 CC disorders such as bipolar disorder, unipolar depression, dysthymia and
 CC seasonal affective disorder, and small cell lung carcinoma.

XX
 SQ Sequence 62 AA;

Query Match

65.5%; Score 36; DB 21; Length 62;

Best Local Similarity 33.3%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPKCXXXXXXC 17
 II I I I
 DB 44 CSHPACSGNNREYC 58

Search completed: January 8, 2003, 15:28:34
 Job time : 31.9394 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 15:27:29 : Search time 11.8485 Seconds
(without alignments)
42.215 Million cell updates/sec

Title: US-09-897-465-1

Perfect score: 55

Sequence: 1 XXCCXPXXXXXXC 17

Scoring table: BLOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	67.3	16	4	US-09-219-446B-4
2	36	65.5	16	2	US-08-857-068-2
3	36	65.5	16	2	US-08-857-068-4
4	36	65.5	16	4	US-09-219-446B-5
5	36	65.5	16	4	US-09-219-446B-8
6	36	65.5	17	4	US-09-219-446B-6
7	36	65.5	19	1	US-08-084-848A-8
8	36	65.5	19	1	US-08-458-499-8
9	35	63.6	16	1	US-08-477-383-54
10	35	63.6	16	1	US-08-487-174-54
11	35	63.6	16	1	US-08-480-750-54
12	35	63.6	16	4	US-09-219-446B-2
13	35	63.6	16	4	US-09-219-446B-11
14	35	63.6	17	4	US-09-219-446B-3
15	35	63.6	19	4	US-09-136-769A-3
16	35	63.6	19	4	US-09-136-769A-14
17	35	63.6	65	1	US-08-137-800-46
18	35	63.6	65	1	US-08-477-383-46
19	35	63.6	65	1	US-08-487-174-46
20	35	63.6	65	1	US-08-480-750-46
21	35	63.6	68	1	US-08-137-800-48
22	35	63.6	68	1	US-08-477-383-48
23	35	63.6	68	1	US-08-487-174-48
24	35	63.6	68	1	US-08-480-750-48
25	34	61.8	16	4	US-09-219-446B-9
26	34	61.8	16	4	US-09-219-446B-12
27	34	61.8	18	1	US-08-137-800-13

28	34	61.8	18	1	US-08-137-800-31	Sequence 31, Appl
29	34	61.8	18	1	US-08-137-800-32	Sequence 32, Appl
30	34	61.8	18	1	US-08-477-383-13	Sequence 13, Appl
31	34	61.8	18	1	US-08-477-383-31	Sequence 31, Appl
32	34	61.8	18	1	US-08-477-383-32	Sequence 32, Appl
33	34	61.8	18	1	US-08-487-174-13	Sequence 13, Appl
34	34	61.8	18	1	US-08-487-174-31	Sequence 31, Appl
35	34	61.8	18	1	US-08-487-174-32	Sequence 32, Appl
36	34	61.8	18	1	US-08-480-750-13	Sequence 13, Appl
37	34	61.8	18	1	US-08-480-750-31	Sequence 31, Appl
38	34	61.8	18	1	US-08-480-750-32	Sequence 32, Appl
39	34	61.8	44	4	US-09-488-799-91	Sequence 91, Appl
40	34	61.8	62	4	US-09-488-799-87	Sequence 87, Appl
41	34	61.8	62	4	US-09-488-799-89	Sequence 89, Appl
42	34	61.8	62	4	US-09-488-799-101	Sequence 101, Appl
43	34	61.8	70	1	US-08-137-800-49	Sequence 49, Appl
44	34	61.8	70	1	US-08-477-383-49	Sequence 49, Appl
45	34	61.8	70	1	US-08-487-174-49	Sequence 49, Appl

ALIGNMENTS

```

RESULT 1
US-09-219-446B-4
; Sequence 4, Application US/09219446B
; Patent No. 6265541
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Sigun
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/219,446B
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PAT derivative
; OTHER INFORMATION: of C. magus MII
US-09-219-446B-4

Query Match
Best Local Similarity 67.3%; Score 37; DB 4; Length 16;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXXPXXXXXXC 17
Db 2 CCSNPVCEATHSMIC 16

RESULT 2
US-08-857-068-2
; Sequence 2, Application US/08857068
; Patent No. 5866682
; GENERAL INFORMATION:
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Cartier, G. Edward
; APPLICANT: Yoshikami, Doju
; APPLICANT: Luo, Sigun
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: CONOPEPTIDES AUA, AUB AND AUC

```

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,068
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-121388
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Conus aulicus
NAME/KEY: Disulfide-bond
LOCATION: 2..8
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 3..16
US-08-857-068-2

Query Match 65.5%; Score 36; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPCXXXXXXC 17
DB 2 CCSYPCFATNSDYC 16

RESULT 3
US-08-857-068-4
Sequence 4, Application US/08857068
Patent No. 5866682
GENERAL INFORMATION:
APPLICANT: McIntosh, J. Michael
APPLICANT: Cartier, G. Edward
APPLICANT: Yoshikami, Doju
APPLICANT: Luo, Siqin
APPLICANT: Oliveira, Baldomero M.
TITLE OF INVENTION: CONOPEPTIDES AUIA, AUIB AND AUIC
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,068
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-121388
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Conus aulicus
NAME/KEY: Disulfide-bond
LOCATION: 2..8
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 3..16
US-08-857-068-4

Query Match 65.5%; Score 36; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPCXXXXXXC 17
DB 2 CCSYPCFATNSDYC 16

RESULT 4
US-09-219-445B-5
Sequence 5, Application US/09219446B
Patent No. 6265541
GENERAL INFORMATION:
APPLICANT: Oliveira, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Siqin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/219,446B
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 16
TYPE: PRT
ORGANISM: Conus aulicus
US-09-219-446B-5

Query Match 65.5%; Score 36; DB 4; Length 16;
Best Local Similarity 33.3%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPCXXXXXXC 17
DB 2 CCSYPCFATNSDYC 16

Query Match	65.5%	Score 36;	DB 4;	Length 17;
Best Local Similarity	33.3%	Pred. No. 11;		
Matches	5;	Conservative	0;	Mismatches 10;
				Indels 0;
				Gaps 0;
QY	3	CCXXPCXXXXXXC	17	

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Db          3  CCSYPCFATNSDYC 17

RESULT 7
US-08-084-848A-8
; Sequence 8, Application US/08084848A
; Patent No. 543155
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Rivier, Jean E. F.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Abogadie, Fe
; APPLICANT: Hopkins, Chris E.
; APPLICANT: Dykert, John
; TITLE OF INVENTION: Conotoxins I
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 South LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/084,848A
; FILING DATE: June 29, 1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Schumann, James J.
; REGISTRATION NUMBER: 20856
; REFERENCE/DOCKET NUMBER: 52511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; TELEX: 20 6566 PATLAW CGO
; INFORMATION FOR SEQ. ID NO.: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
;
US-08-084-848A-8

Query Match          65.5%; Score 36; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY          3  CCXXPCXXXXXXXC 17
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Db          2  CCSHPACSGKXQXC 16

RESULT 8
US-08-458-499-8
; Sequence 8, Application US/08458499
; Patent No. 5700778
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Rivier, Jean E. F.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Abogadie, Fe
; APPLICANT: Hopkins, Chris E.
; APPLICANT: Dykert, John
; APPLICANT: Torres, Josep L.
; TITLE OF INVENTION: Conotoxins I
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 South LaSalle Street, Suite 900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,499
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/084,848
FILING DATE: June 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Schumann, James J.
REGISTRATION NUMBER: 20856
REFERENCE/DOCKET NUMBER: 52511
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)552-1311
TELEFAX: (619)552-0095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-458-499-8

Query Match 65.5%; Score 36; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
DB 2 CSHPCSGKXYXC 16

RESULT 9
US-08-477-383-54
Sequence 54, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800

FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus magus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 16
OTHER INFORMATION: /note="The C-terminus is
OTHER INFORMATION: amidated."
US-08-477-383-54

Query Match 63.6%; Score 35; DB 1; Length 16;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
DB 2 CCNPVCHLSNLC 16

RESULT 10
US-08-487-174-54
Sequence 54, Application US/08487174
Patent No. 5595972
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.

```

RESULT 12
US-09-219-446B-2
; Sequence 2, Application US/09219446B
; Patent No. 6265541
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Sigin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/219,446B
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus magus
US-09-219-446B-2

Query Match          63.6%; Score 35; DB 4; Length 16;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      3 CCXXPCXXXXXXC 17
        || | |
Db       2 CCSNPSCHLHSHNLC 16

RESULT 13
US-09-219-446B-11
; Sequence 11, Application US/09219446B
; Patent No. 6265541
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Sigin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

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; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/219,446B
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 11
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: N1LS derivative
; OTHER INFORMATION: of C. purpurascens Pn1A
US-09-219-446B-11

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Query Match      63.6%; Score 35; DB 4; Length 16;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY      3 CCXXPCXXXXXXC 17
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DB      2 CCSLPCCASNPYC 16

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RESULT 14
US-09-219-446B-3
; Sequence 3, Application US/09219446B
; Patent No. 6265541
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/219,446B
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tyr derivative
; OTHER INFORMATION: of C. magus M11
US-09-219-446B-3

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Query Match      63.6%; Score 35; DB 4; Length 17;
Best Local Similarity 33.3%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY      3 CCXXPCXXXXXXC 17
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DB      3 CCSPVCHLSHSLC 17

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RESULT 15
US-09-136-769A-3
; Sequence 3, Application US/09136769A
; Patent No. 6307014
; GENERAL INFORMATION:
; APPLICANT: Furie, Bruce
; APPLICANT: Furie, Barbara

```

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; APPLICANT: Stenflo, Johan
; APPLICANT: Raby, Alan C.
; APPLICANT: Roepstorff, Peter
; TITLE OF INVENTION: CONOPEPTIDES
; FILE REFERENCE: 50065/002001
; CURRENT APPLICATION NUMBER: US/09/136,769A
; CURRENT FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Conus textile
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)...(16)
; OTHER INFORMATION: Pro at position 2 is 4Hyp and each Xaa is
; OTHER INFORMATION: Independently selected from Glu and
; OTHER INFORMATION: gamma-carboxyglutamic acid, provided that at least
; OTHER INFORMATION: one Xaa is gamma-carboxyglutamic acid.
; NAME/KEY: VARIANT
; LOCATION: (1)...(19)
; OTHER INFORMATION: Xaa = Any Amino Acid
; NAME/KEY: VARIANT
; LOCATION: (1)...(19)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-136-769A-3

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Query Match      63.6%; Score 35; DB 4; Length 19;
Best Local Similarity 40.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY      3 CCXXPCXXXXXXC 17
      1 1 1 1 1
DB      4 CCSDPCNSSHPLC 18

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 8, 2003, 15:30:00 ; Search time 7.72727 Seconds
(without alignments)
42.682 Million cell updates/sec

Title: US-09-897-465-1

Perfect score: 55

Sequence: 1 XXCCXPXCXXXXXXC 17

Scoring table: BLOSUM62

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA:*
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10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	36	65.5	16	10	US-09-897-465-8
4	36	65.5	17	10	US-09-897-465-6
5	35	63.6	16	10	US-09-897-465-2
6	35	63.6	16	10	US-09-897-465-11
7	35	63.6	17	10	US-09-897-465-3
8	34	61.8	16	10	US-09-897-465-9
9	34	61.8	16	10	US-09-897-465-12
10	34	61.8	4679	10	US-09-804-898-2
11	33	60.0	16	10	US-09-897-465-10
12	33	60.0	17	10	US-09-897-465-1
13	33	60.0	480	10	US-09-823-936-16
14	32	58.2	12	10	US-09-897-465-13
15	32	58.2	85	10	US-09-864-761-39564
16	32	58.2	134	10	US-09-864-761-39564
17	32	58.2	141	9	US-09-970-966-215
18	32	58.2	141	10	US-09-825-294-215
19	32	58.2	288	10	US-09-323-998B-19

20	32	58.2	352	9	US-09-978-295A-612	Sequence 612, App
21	32	58.2	352	9	US-09-978-697-612	Sequence 612, App
22	32	58.2	352	9	US-09-978-192A-612	Sequence 612, App
23	32	58.2	352	9	US-09-999-832A-612	Sequence 612, App
24	32	58.2	352	9	US-09-978-189-612	Sequence 612, App
25	32	58.2	354	9	US-10-066-500-130	Sequence 130, App
26	32	58.2	516	10	US-09-908-670-3	Sequence 3, App1
27	32	58.2	4440	12	US-10-052-586-325	Sequence 525, App
28	31	56.4	15	10	US-09-897-465-7	Sequence 79, App1
29	31	56.4	51	10	US-09-864-761-43103	Sequence 43103, A
30	31	56.4	70	10	US-09-739-254-79	Sequence 24, App1
31	31	56.4	70	10	US-09-904-615-79	Sequence 79, App1
32	31	56.4	73	10	US-09-764-877-1910	Sequence 1910, Ap
33	31	56.4	75	9	US-10-138-516-6	Sequence 6, App1
34	31	56.4	75	9	US-10-146-130-8	Sequence 8, App1
35	31	56.4	192	9	US-10-095-139-12	Sequence 12, App1
36	31	56.4	585	10	US-09-817-774-24	Sequence 24, App1
37	31	56.4	1184	12	US-10-153-064-89	Sequence 89, App1
38	31	56.4	1422	10	US-09-735-933-1	Sequence 2, App1
39	31	56.4	1497	10	US-09-060-854B-2	Sequence 82, App1
40	31	56.4	2771	9	US-09-808-602-82	Sequence 24, App1
41	31	56.4	3907	9	US-10-029-217A-24	Sequence 45446, A
42	30	54.5	62	10	US-09-864-761-45446	Sequence 971, App
43	30	54.5	74	10	US-09-731-242A-4	Sequence 110, App
44	30	54.5	76	10	US-09-764-869-971	
45	30	54.5	122	10	US-09-789-561-110	

ALIGNMENTS

RESULT 1
US-09-897-465-4
Sequence 4, Application US/09897465
Patent No. US2002022715A1
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Siqin
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/897,465
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: FAT derivative
OTHER INFORMATION: of C. magus MII
US-09-897-465-4
Query Match 67.3%; Score 37; DB 10; Length 16;
Best Local Similarity 33.3%; Pred. No. 9.2;
Matches 5; Conservatve 0; Mismatches 10; Indels 0; Gaps 0;
QY 3 CCXXPCXXXXXXC 17
Db 2 CCSPVCFATHSNLC 16
RESULT 2
US-09-897-465-5
Sequence 5, Application US/09897465

Patent No. US20020022715A1
: GENERAL INFORMATION:
: APPLICANT: Olivera, Baldomero M.
: APPLICANT: McIntosh, J. Michael
: APPLICANT: Yoshikami, Doju
: APPLICANT: Cartier, G. Edward
: APPLICANT: Luo, Siglin
: APPLICANT: University of Utah Research Foundation
: TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
: FILE REFERENCE: Uses of Alpha-Conotoxins
: CURRENT APPLICATION NUMBER: US/09/897,465
: CURRENT FILING DATE: 2001-07-03
: PRIOR APPLICATION NUMBER: US 60/080,588
: PRIOR FILING DATE: 1998-04-03
: PRIOR APPLICATION NUMBER: US 60/070,153
: PRIOR FILING DATE: 1997-12-31
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 5
: LENGTH: 16
: TYPE: PRF
: ORGANISM: Conus aulicus
US-09-897-465-5

Query Match 65.5%; Score 36; DB 10; Length 16;
Best Local Similarity 33.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXKXXXXXC 17
Db 2 CCXXPCFATNSDYC 16

RESULT 3
US-09-897-465-8
: Sequence 8, Application US/09897465
: Patent No. US20020022715A1
: GENERAL INFORMATION:
: APPLICANT: Olivera, Baldomero M.
: APPLICANT: McIntosh, J. Michael
: APPLICANT: Yoshikami, Doju
: APPLICANT: Cartier, G. Edward
: APPLICANT: Luo, Siglin
: APPLICANT: University of Utah Research Foundation
: TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
: FILE REFERENCE: Uses of Alpha-Conotoxins
: CURRENT APPLICATION NUMBER: US/09/897,465
: CURRENT FILING DATE: 2001-07-03
: PRIOR APPLICATION NUMBER: US 60/080,588
: PRIOR FILING DATE: 1998-04-03
: PRIOR APPLICATION NUMBER: US 60/070,153
: PRIOR FILING DATE: 1997-12-31
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 8
: LENGTH: 16
: TYPE: PRF
: ORGANISM: Conus aulicus
US-09-897-465-8

Query Match 65.5%; Score 36; DB 10; Length 16;
Best Local Similarity 33.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXKXXXXXC 17
Db 2 CCXXPCFATNSGYC 16

RESULT 4
US-09-897-465-6
: Sequence 6, Application US/09897465
: Patent No. US20020022715A1

: GENERAL INFORMATION:
: APPLICANT: Olivera, Baldomero M.
: APPLICANT: McIntosh, J. Michael
: APPLICANT: Yoshikami, Doju
: APPLICANT: Cartier, G. Edward
: APPLICANT: Luo, Siglin
: APPLICANT: University of Utah Research Foundation
: TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
: FILE REFERENCE: Uses of Alpha-Conotoxins
: CURRENT APPLICATION NUMBER: US/09/897,465
: CURRENT FILING DATE: 2001-07-03
: PRIOR APPLICATION NUMBER: US 60/080,588
: PRIOR FILING DATE: 1998-04-03
: PRIOR APPLICATION NUMBER: US 60/070,153
: PRIOR FILING DATE: 1997-12-31
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 6
: LENGTH: 17
: TYPE: PRF
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Tyr derivative
US-09-897-465-6

Query Match 65.5%; Score 36; DB 10; Length 17;
Best Local Similarity 33.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXKXXXXXC 17
Db 3 CCXXPCFATNSDYC 17

RESULT 5
US-09-897-465-2
: Sequence 2, Application US/09897465
: Patent No. US20020022715A1
: GENERAL INFORMATION:
: APPLICANT: Olivera, Baldomero M.
: APPLICANT: McIntosh, J. Michael
: APPLICANT: Yoshikami, Doju
: APPLICANT: Cartier, G. Edward
: APPLICANT: Luo, Siglin
: APPLICANT: University of Utah Research Foundation
: TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
: FILE REFERENCE: Uses of Alpha-Conotoxins
: CURRENT APPLICATION NUMBER: US/09/897,465
: CURRENT FILING DATE: 2001-07-03
: PRIOR APPLICATION NUMBER: US 60/080,588
: PRIOR FILING DATE: 1998-04-03
: PRIOR APPLICATION NUMBER: US 60/070,153
: PRIOR FILING DATE: 1997-12-31
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 2
: LENGTH: 16
: TYPE: PRF
: ORGANISM: Conus magus
US-09-897-465-2

Query Match 63.6%; Score 35; DB 10; Length 16;
Best Local Similarity 33.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXKXXXXXC 17
Db 2 CCXNPVCHLEHSLC 16

RESULT 6
US-09-897-465-11

```

; Sequence 11, Application US/09897465
; Patent No. US2002022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siqin
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NLS derivative
; OTHER INFORMATION: of C. purpurascens PnIA
US-09-897-465-11

```

```

Query Match          63.6%; Score 35; DB 10; Length 16;
Best Local Similarity 33.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

```

Qy 3 CCXXPCXKXXXXXXC 17
Db 2 CCLSPPCASNPDYC 16

```

```

RESULT 7
; Sequence 3, Application US/09897465
; Patent No. US2002022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siqin
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tyr derivative
; OTHER INFORMATION: of C. magus MII
US-09-897-465-3

```

```

Query Match          63.6%; Score 35; DB 10; Length 17;
Best Local Similarity 33.3%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

```

Qy 3 CCXXPCXKXXXXXXC 17
Db 2 CCLSPPCASNPDYC 16

```

```

Db 3 CCSPVCHLSNLC 17
RESULT 8
; Sequence 9, Application US/09897465
; Patent No. US2002022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siqin
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-09-897-465-9

```

```

Query Match          61.8%; Score 34; DB 10; Length 16;
Best Local Similarity 33.3%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

```

Qy 3 CCXXPCXKXXXXXXC 17
Db 2 CCLSPPCASNPDYC 16

```

```

RESULT 9
; Sequence 12, Application US/09897465
; Patent No. US2002022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siqin
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-09-897-465-12

```

```

Query Match          61.8%; Score 34; DB 10; Length 16;
Best Local Similarity 33.3%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

```

Qy 3 CCXXPCXKXXXXXXC 17
Db 2 CCLSPPCASNPDYC 16

```

```
RESULT 10
; US-09-804-898-2
; Sequence 2, Application US/09804898
; Patent No. US20020045264A1
; GENERAL INFORMATION:
; APPLICANT: DURING, MATTHEW
; APPLICANT: XIAO, WEIDONG
; TITLE OF INVENTION: PRODUCTION OF CHIMERIC CAPSID VECTORS
; FILE REFERENCE: 102182-14
; CURRENT APPLICATION NUMBER: US/09/804,898
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/189,110
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4679
; TYPE: PRT
; ORGANISM: adeno-associated virus 2
; US-09-804-898-2
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Query Match          61.8%; Score 34; DB 10; Length 4679;
Best Local Similarity 26.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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QY      3 CCXXPXCCXXXXXXC 17
      11 | | | | | | | | | |
Db      1910 CCAAAACAATGTTG 1924
```

```
RESULT 11
; US-09-897-465-10
; Sequence 10, Application US/09897465
; Patent No. US20020022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A10L derivative
; OTHER INFORMATION: of C. purpurascens Pn1A
; US-09-897-465-10
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```
Query Match          60.0%; Score 33; DB 10; Length 16;
Best Local Similarity 33.3%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
QY      3 CCXXPXCCXXXXXXC 17
      11 | | | | | | | | | |
Db      2 CCSLPPCALNNPDYC 16
```

```
RESULT 12
US-09-897-465-1
```

```
; Sequence 1, Application US/09897465
; Patent No. US20020022715A1
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/897,465
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: generic
; OTHER INFORMATION: alpha-conotoxin sequence
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(6)
; OTHER INFORMATION: Xaa at residue 1 is des-Xaa, Tyr, mono-Iodo-Tyr or
; OTHER INFORMATION: di-Iodo-Tyr; Xaa at residue 2 is any amino acid;
; OTHER INFORMATION: Xaa at residue 5 is any amino acid; Xaa at residue
; NAME/KEY: PEPTIDE
; LOCATION: (8)-(12)
; OTHER INFORMATION: Xaa at residues 8, 10, 11 and 12 may be any amino
; OTHER INFORMATION: acid; Xaa at residues 13, 14, 15 and 16 may be
; OTHER INFORMATION: des-Xaa or any amino acid.
; US-09-897-465-1
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```
Query Match          60.0%; Score 33; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      3 CCXXPXCCXXXXXXC 17
      11 | | | | | | | | | |
Db      3 CCXXPXCCXXXXXXC 17
```

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RESULT 13
; US-09-823-936-16
; Sequence 16, Application US/09823936
; Patent No. US20020061309A1
; GENERAL INFORMATION:
; APPLICANT: GARGER, Stephen J.
; APPLICANT: GROSS, Cynthia
; APPLICANT: LINDBO, John A.
; APPLICANT: POCUE, Gregory P.
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS
; TITLE OF INVENTION: N-TERMINAL VIRAL COAT PROTEIN FUSIONS
; FILE REFERENCE: 008010087CPOS05
; CURRENT APPLICATION NUMBER: US/09/823,936
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 09/520,967
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 480
; TYPE: PRT
; ORGANISM: P. Yoeli
; US-09-823-936-16
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Query Match          60.0%; Score 33; DB 10; Length 480;
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Best Local Similarity 26.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3 CCXXPXCXXXXXXC 17

DB 410 CCGGATCTTATATATC 424

RESULT 14

US-09-897-465-13

Sequence 13, Application US/09897465

Patent No. US20020022715A1

GENERAL INFORMATION:

APPLICANT: Oliveira, Baldomero M.

APPLICANT: McIntosh, J. Michael

APPLICANT: Yoshikami, Doju

APPLICANT: Carlier, G. Edward

APPLICANT: Luo, Siqin

APPLICANT: University of Utah Research Foundation

TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

FILE REFERENCE: Uses of Alpha-Conotoxins

CURRENT APPLICATION NUMBER: US/09/897,465

CURRENT FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: US 60/080,588

PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: US 60/070,153

PRIOR FILING DATE: 1997-12-31

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 13

LENGTH: 12

TYPE: PRT

ORGANISM: *Conus imperialis*

US-09-897-465-13

Query Match 58.2%; Score 32; DB 10; Length 12;
Best Local Similarity 57.1%; Pred. No. 39;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCXXPXC 9

DB 2 CCSDPXC 8

RESULT 15

US-09-864-761-39864

Sequence 39864, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aecm1ca-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 39864

LENGTH: 85

TYPE: PRT

ORGANISM: *Homo sapiens*

FEATURE:

OTHER INFORMATION: MAP TO AC006070.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4

US-09-864-761-39864

QY 3 CCXXPXC 9

DB 76 CCSTPXC 82

Search completed: January 8, 2003, 15:36:36

Job time: 7.72727 secs

Query Match 58.2%; Score 32; DB 10; Length 85;
Best Local Similarity 57.1%; Pred. No. 95;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 8, 2003, 15:27:14 ; Search time 13.9091 Seconds
(without alignments)
117.498 Million cell updates/sec

Title: US-09-897-465-1

Perfect score: 55

Sequence: 1 XXXCCXPXXXXXXC 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	65.5	16	2 C59045	alpha-conotoxin Au
2	36	65.5	16	2 A59045	alpha-conotoxin Au
3	35	63.6	16	2 A59046	alpha-conotoxin Mi
4	34	61.8	16	2 A54877	alpha-conotoxin Pn
5	34	61.8	16	2 B54877	alpha-conotoxin Pn
6	34	61.8	18	1 A58589	alpha-conotoxin Ei
7	33	60.0	16	2 A59042	alpha-conotoxin Ep
8	33	60.0	52	2 JCI197	metallothionein II
9	33	60.0	169	2 T42115	transposase - Esch
10	33	60.0	197	2 T10081	sperm mitochondria
11	33	60.0	223	2 B58346	ultra-high-sulfur
12	33	60.0	230	2 A38346	ultra-high-sulfur
13	33	60.0	363	2 A48338	hypothetical prote
14	33	60.0	426	2 S23782	transposase tmpr (
15	33	60.0	535	2 S56261	probable membrane
16	33	60.0	542	2 I39540	chitinase (EC 3.2.
17	33	60.0	782	2 A61625	tenascin-like prot
18	33	58.2	12	1 A53709	alpha-conotoxin Im
19	32	58.2	113	2 S67020	probable membrane
20	32	58.2	149	2 T46937	hypothetical prote
21	32	58.2	172	2 I47106	high-sulfur wool m
22	32	58.2	197	2 T15725	keratin KAP5.5 - s
23	32	58.2	210	2 B82522	hypothetical prote
24	32	58.2	210	2 B82522	hypothetical prote
25	32	58.2	288	2 A34440	isopentenyl-diphos
26	32	58.2	321	2 F71483	probable dipeptide
27	32	58.2	321	2 C81746	peptide ABC transp
28	32	58.2	368	2 T21748	hypothetical prote
29	32	58.2	419	1 WJFPH2	homeotic protein H

30	32	58.2	422	2 D86445	hypothetical prote
31	32	58.2	516	2 S19586	N-methyl-D-asparta
32	32	58.2	516	2 T39979	probable zinc fing
33	32	58.2	607	2 S49528	endoxylanase - rum
34	32	58.2	607	2 T23874	endo-1,4-beta-xyla
35	32	58.2	635	2 T23874	hypothetical prote
36	32	58.2	1101	2 T16840	hypothetical prote
37	32	58.2	1152	2 H86486	hypothetical prote
38	32	58.2	1267	2 T21340	protein ty1/copia-
39	31	56.4	15	2 B59045	hypothetical prote
40	31	56.4	19	2 A44379	alpha-conotoxin Au
41	31	56.4	90	2 D85845	alpha-conotoxin SI
42	31	56.4	151	2 S60314	probable lysis pro
43	31	56.4	152	1 KRSHHC	hair keratin cyste
44	31	56.4	152	2 I47109	keratin high-sulfu
45	31	56.4	152	2 I47111	high-sulfur wool m

ALIGNMENTS

RESULT 1

C59045 alpha-conotoxin Aulic - cone shell (Conus aulicus)

C:Species: Conus aulicus (Court cone)

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C:Accession: C59045

R:Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.;

J. Neurosci. 18, 8571-8579, 1998

A:Title: Alpha-conotoxin AulB selectively blocks alpha3beta4 nicotinic acetylcholine

A:Reference number: A59045; MWID:99003392; PMID:9786965

A:Accession: C59045

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <LUO>

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F:1-16/Product: alpha-conotoxin AulB #status experimental <MAT>

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 65.5%; Score 36; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPCXXXXXXC 17
DB 2 CCSTPCFATNSGYC 16

RESULT 2

A59045 alpha-conotoxin AulA - cone shell (Conus aulicus)

C:Species: Conus aulicus (Court cone)

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C:Accession: A59045

R:Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.;

J. Neurosci. 18, 8571-8579, 1998

A:Title: Alpha-conotoxin AulB selectively blocks alpha3beta4 nicotinic acetylcholine

A:Reference number: A59045; MWID:99003392; PMID:9786965

A:Accession: A59045

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <LUO>

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F:1-16/Product: alpha-conotoxin AulA #status experimental <MAT>

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 65.5%; Score 36; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
DB 2 CCSPPCPCATNSDYC 16

RESULT 3

A:Accession: A59046
A:Title: alpha-conotoxin MII - cone shell (Conus magus)
C:Species: Conus magus (magus cone)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: A59046
R:Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.
J. Biol. Chem. 271, 7522-7528, 1996
A:Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine receptor
A:Reference number: A59046; MUID:96205934; PMID:8631783
A:Accession: A59046
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <CAR>
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
F:1-16/Product: alpha-conotoxin MII #status experimental <MAT>
F:2-8,3-16/Disulfide bonds: #status experimental
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 63.6%; Score 35; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
DB 2 CCSNPVCHLSNLC 16

RESULT 4

A54877
A:Accession: A54877
A:Title: alpha-conotoxin PnIA [validated] - cone shell (Conus pennaceus)
N:Alternate names: alpha-Cnx-PnIA
C:Species: Conus pennaceus
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
C:Accession: A54877
R:Faingold, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlotk
Biochemistry 33, 9523-9529, 1994
A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rece
A:Reference number: A54877; MUID:94347719; PMID:8068627
A:Accession: A54877
A:Molecule type: protein
A:Residues: 1-16 <FAI>
R:Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.
submitted to the Brookhaven Protein Data Bank, January 1996
A:Reference number: A66355; PDB:1PEN
A:Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
F:2-8,3-16/Disulfide bonds: #status experimental
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 61.8%; Score 34; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
DB 2 CCSLPPCANPNPYC 16

RESULT 5

B54877
A:Accession: A54877
A:Title: alpha-conotoxin PnIB - cone shell (Conus pennaceus)
C:Species: Conus pennaceus
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-May-1997

C:Accession: B54877
R:Faingold, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zl
Biochemistry 33, 9523-9529, 1994
A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine r
A:Reference number: A54877; MUID:94347719; PMID:8068627
A:Accession: B54877
A:Molecule type: protein
A:Residues: 1-16 <FAI>
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu
F:2-8,3-16/Disulfide bonds: #status experimental
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 61.8%; Score 34; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
DB 2 CCSLPPCANPNPYC 16

RESULT 6

A58589
A:Accession: A58589
A:Title: alpha-conotoxin EI - cone shell (Conus ermineus)
C:Species: Conus ermineus (ermine cone)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A58589
R:Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Craik, A.G.; Groebe, D.R.; Abramson, S.N
Biochemistry 34, 14519-14526, 1995
A:Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with n
A:Reference number: A58589; MUID:96062516; PMID:7578057
A:Accession: A58589
A:Molecule type: protein
A:Residues: 1-18 <MAR>
A:Note: sequence confirmed by chemical synthesis
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline;
F:4-10,5-18/Disulfide bonds: #status experimental
F:18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 61.8%; Score 34; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
DB 4 CCVHPTCNMSNPQIC 18

RESULT 7

A59042
A:Accession: A59042
A:Title: alpha-conotoxin EPI - cone shell (Conus episcopatus)
C:Species: Conus episcopatus (bishop's cone)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 13-Aug-1999
C:Accession: A59042
R:Loughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett,
J. Biol. Chem. 273, 15667-15674, 1998
A:Title: Alpha-conotoxin EPI, a novel sulfated peptide from Conus episcopatus that se
A:Reference number: A59042; MUID:98288307; PMID:9624161
A:Accession: A59042
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <LOU>
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu
F:1-16/Product: alpha-conotoxin EPI #status experimental <MAT>
F:2-8,3-16/Disulfide bonds: #status experimental
F:15/Binding site: sulfated (Tyr) (covalent) #status experimental
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

A:Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin
A:Reference number: A38346; MUID:91065960; PMID:2250030
A:Accession: B38346
A:Molecule type: DNA
A:Residues: 1-21, 'GGCGSGCGGCGSGGCGSSCKPVC', 22-40, 'GSS', 44-45, 'G', 47-48, 'S', 50, 'GSS',
<MOO>
A:Cross-references: GB:M37759; NID:g200961; PIDN:AAA0106.1; PID:g200962
A:Note: the sequence reported in this paper has been corrected. See A38660
C:Superfamily: ultra-high-sulfur keratin

Query Match 60.0%; Score 33; DB 2; Length 223;
Best Local Similarity 33.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
DB 26 CCCVPVCCSSCGGC 40

RESULT 12

A38346
ultra-high-sulfur keratin 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999
R:Wood, L.; Mills, M.; Hatzenbuehler, N.; Vogel, G.
J. Biol. Chem. 265, 21375-21380, 1990
A:Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin
A:Reference number: A38346; MUID:91065960; PMID:2250030
A:Accession: A38346
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <MOO>
A:Cross-references: GB:M37759; NID:g200961; PIDN:AAA0106.1; PID:g200962
C:Superfamily: ultra-high-sulfur keratin

Query Match 60.0%; Score 33; DB 2; Length 230;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
DB 53 CCCVPVCCSSCGGC 67

RESULT 13

A48338
hypothetical protein orf67 - equine herpesvirus 4 (strain 405/76)
C:Species: equine herpesvirus 4
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 08-Oct-1999
C:Accession: A48338
R:Nagesha, H.S.; Crabb, B.S.; Studdert, M.J.
Arch. Virol. 128, 143-154, 1993
A:Title: Analysis of the nucleotide sequence of five genes at the left end of the unique
A:Reference number: A48338; MUID:93119267; PMID:8380320
A:Accession: A48338
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-363 <NAG>
A:Cross-references: GB:M89634; NID:g330929; PIDN:AAA46100.1; PID:g330930
A:Note: sequence extracted from NCBI backbone (NCBIN:121741, NCBIR:121742)

Query Match 60.0%; Score 33; DB 2; Length 363;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CCXXPC 9
DB 285 CCLTPAC 291

RESULT 14

S23782

transposase tnpA (insertion sequence IS91) - Escherichia coli
C:Species: Escherichia coli
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 10-Dec-1999
C:Accession: S23782
R:Mendola, M.V.; Jubete, Y.; de la Cruz, F.
J. Bacteriol. 174, 1345-1351, 1992
A:Title: DNA sequence of IS91 and identification of the transposase gene.
A:Reference number: S23781; MUID:92138630; PMID:1310503
A:Accession: S23782
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <MEN>
A:Cross-references: EMBL:X17114; NID:g41840; PIDN:CAA34970.1; PID:g41842
C:Genetics:
A:Gene: tnpA
A:Mobile element: insertion sequence IS91
C:Superfamily: Escherichia IS91 transposase tnpA

Query Match 60.0%; Score 33; DB 2; Length 426;
Best Local Similarity 57.1%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CCXXPC 9
DB 52 CCSPPC 58

RESULT 15

S56261
probable membrane protein YFR006w - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 19-Apr-2002
C:Accession: S56261
R:Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasamura, S.I.; Sas
submitted to the EMBL Data Library, May 1995
A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces
A:Reference number: S56186
A:Accession: S56261
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-535 <MUR>
A:Cross-references: EMBL:D50617; NID:g836685; PID:d1009886; PID:g836761; MIPS:YFR006w
C:Genetics:
A:Cross-references: SGD:S0001902
A:Map position: 6R
C:Keywords: transmembrane protein
F:5-21/Domain: transmembrane #status predicted <TM>

Query Match 60.0%; Score 33; DB 2; Length 535;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CCXXPC 9
DB 289 CCSPAC 295

Search completed: January 8, 2003, 15:30:27
Job time : 15.9091 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 8, 2003, 15:24:24 ; Search time 7.72727 Seconds
(Without alignments)
91.248 Million cell updates/sec

Title: US-09-897-465-1
Perfect score: 55
Sequence: 1 XXCCXXPCFATNSDYC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSPROT.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	36	65.5	16 1	CXA1.CONAL
2	36	65.5	16 1	CXA3.CONAL
3	35	63.6	16 1	CXA2.CONAL
4	35	63.6	69 1	CXA1.CONTE
5	35	63.6	194 1	KRUB.HUMAN
6	34	61.8	16 1	CXA4.CONPE
7	34	61.8	16 1	CXA8.CONPE
8	34	61.8	18 1	CXA1.CONER
9	34	61.8	19 1	CXR.CONTU
10	34	61.8	66 1	CXA2.CONTE
11	33	60.0	16 1	CXA1.CONEP
12	33	60.0	51 1	MT2.CANGA
13	33	60.0	197 1	MCS.MOUSE
14	33	60.0	535 1	YFHB.YEAST
15	33	58.2	12 1	CXA1.CONIM
16	32	58.2	231 1	FLGH.PSEPU
17	32	58.2	287 1	ID11.YEAST
18	32	58.2	368 1	CCR3.HUMAN
19	32	58.2	410 1	HMH2.DROME
20	32	58.2	607 1	XYNA.NEOPA
21	31	56.4	15 1	CXA2.CONAL
22	31	56.4	72 1	CXA2.CONST
23	31	56.4	151 1	KR2C.SHEEP
24	31	56.4	156 1	KR2B.SHEEP
25	31	56.4	158 1	VE6.HPV39
26	31	56.4	169 1	KRUA.HUMAN
27	31	56.4	171 1	KR2A.SHEEP
28	31	56.4	181 1	KR2D.SHEEP
29	31	56.4	182 1	KRUC.SHEEP
30	31	56.4	191 1	VE6.RHPV1
31	31	56.4	194 1	FLR.DESGI
32	31	56.4	271 1	RCE1.SCHPO
33	31	56.4	287 1	PDC2.RAT

34	31	56.4	339 1	CMC2.YEAST	012046 saccharomyc
35	31	56.4	343 1	PDC2.MOUSE	P46718 mus musculu
36	31	56.4	489 1	YM20.YEAST	P40210 saccharomyc
37	30	54.5	692 1	ANMX.HUMAN	Q9avm4 homo sapien
38	30	54.5	692 1	ANMX.MOUSE	Q922x9 mus musculu
39	30	54.5	729 1	ANMX.CRILLO	Q99m19 cricetulus
40	30	54.5	817 1	DLG3.HUMAN	Q92796 homo sapien
41	30	54.5	849 1	DLG3.MOUSE	P70175 mus musculu
42	30	54.5	849 1	DLG3.RAT	Q62936 rattus norv
43	29	52.7	99 1	NIC1.HUMAN	Q9ug19 homo sapien
44	29	52.7	225 1	PRR3.JUNAS	P81295 juniperus a
45	29	52.7	571 1	DIST.BOTVA	P30431 bothriops ja

ALIGNMENTS

RESULT 1	ID	CXA1.CONAL	STANDARD:	PRT:	16 AA.
AC	P56639;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Alpha-conotoxin AUIA.				
OS	Conus aulicus (Court cone).				
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;				
OC	Neogastropoda; Conoidea; Conidae; Conus.				
ON	NCBI_TaxID=89437;				
RN	[1]				
RP	SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.				
RC	TISSUE-Venom.				
RX	MEDLINE=99003392; PubMed=9786965;				
RA	Luo S., Kulak J.M., Carlier G.E., Jacobsen R.B., Yoshikami D.,				
RA	Olivera B.M., McIntosh J.M.;				
RT	"Alpha-conotoxin AUIB selectively blocks alpha3 beta4 nicotinic				
RT	acetylcholine receptors and nicotine-evoked norepinephrine release.";				
RL	J. Neurosci. 18:8571-8579(1998).				
CC	- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES. THEY				
CC	BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS				
CC	INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC				
CC	ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.				
CC	- SUBCELLULAR LOCATION: Secreted.				
CC	- TISSUE SPECIFICITY: Expressed by the venom duct.				
CC	- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray				
CC	- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE				
CC	FAMILY.				
DR	HSSP; P50984; 1PEN.				
KW	Postsynaptic neurotoxin; Neurotoxin; Toxin;				
KW	Acetylcholine receptor inhibitor; Amidation.				
FT	DISULFID 2 8				
FT	DISULFID 3 16				
FT	MOD.RES 16 16				
SQ	SEQUENCE 16 AA; 1731 MW; 1E310FB8FFDC7001 CRC64;				
QY	3 CCXXPCFATNSDYC 17				
Db	2 CCSTPCFATNSDYC 16				
Query Match	65.5%; Score 36; DB 1; Length 16;				
Best local Similarity	33.3%; Pred. No. 4.4;				
Matches	5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;				
RESULT 2					
ID	CXA3.CONAL	STANDARD:	PRT:	16 AA.	
AC	P56641;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Alpha-conotoxin AUIA.				
OS	Conus aulicus (Court cone).				

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxId=89437;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE-Venom;
 RX MEDLINE=99003392; PubMed=9786965;
 RA Luo S., Kulak J.M., Carlier G.E., Jacobsen R.B., Yoshikami D.,
 RA Olivera B.M., McIntosh J.M.;
 RT "Alpha-conotoxin Aurb selectively blocks alpha3 beta2 nicotinic
 acetylcholine receptors and nicotine-evoked norepinephrine release."
 RL J. Neurosci. 18:8571-8579(1998).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
 ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1667.6; METHOD-Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 FAMILY.
 DR HSSP: p50984; 1PEN.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD.RES 16 16
 SQ SEQUENCE 16 AA; 1673 MW; 1E310D3B8FDC7001 CRC64;
 AMIDATION.

Query Match 65.5%; Score 36; DB 1; Length 16;
 Best Local Similarity 33.3%; Pred. No. 4.4;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
 Db 2 CCSTPCFATNSGYC 16

RESULT 3
 CXAL_CONTE STANDARD; PRT; 16 AA.
 ID CXAL_CONTE
 AC P56636;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin MII (M2).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxId=6492;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Venom;
 RX MEDLINE=96205934; PubMed=8631783;
 RA Carlier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
 RA McIntosh J.M.;
 RT "A new alpha-conotoxin which targets alpha3beta2 nicotinic
 acetylcholine receptors."
 RL J. Biol. Chem. 271:7522-7528(1996).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=98062282; PubMed=9398298;
 RA Shon K.-I., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;
 RT "Three-dimensional solution structure of alpha-conotoxin MII, an
 alpha3beta2 neuronal nicotinic acetylcholine receptor-targeted
 ligand."
 RL Biochemistry 36:15693-15700(1997).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99060038; PubMed=9843366;
 RA Hill J.M., Oomen C.J., Miranda L.P., Bingham J.-P., Alewood P.F.,
 RA Craik D.J.;
 RT "Three-dimensional solution structure of alpha-conotoxin MII by NMR

RT spectroscopy: effects of solution environment on helicity.";
 RL Biochemistry 37:15621-15630(1998).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
 ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS. IT
 HAS AN ACTIVITY 2 TO 4 ORDERS OF MAGNITUDE LESS POTENT ON OTHER
 NACHR SUBUNIT COMBINATIONS.
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 FAMILY.
 DR PDB: 1MI1; 21-OCT-98.
 DR PDB: 1M3C; 13-JAN-99.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD.RES 16 16
 SQ SEQUENCE 16 AA; 1716 MW; 282AEF190166CAF9 CRC64;
 AMIDATION.

Query Match 63.6%; Score 35; DB 1; Length 16;
 Best Local Similarity 33.3%; Pred. No. 6.1;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
 Db 2 CCSTPCFATNSGYC 16

RESULT 4
 CXAL_CONTE STANDARD; PRT; 69 AA.
 ID CXAL_CONTE
 AC Q9XZK6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-type conotoxin Tx1 precursor.
 OS Conus textile (Cloth-of-gold cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxId=6494;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Venom duct;
 RX MEDLINE=20037955; PubMed=10573284;
 RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
 RT "Conopeptides from Conus striatus and Conus textile by cDNA
 cloning."
 RL Peptides 20:1139-1144(1999).
 CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 bind to the nicotinic acetylcholine receptors (nAChR) and thus
 inhibit them (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 FAMILY.

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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF146352; AAD31912.1; -
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Signal; Amidation.
 FT SIGNAL 1 21
 FT PROPEP 22 48
 FT PEPTIDE 49 66
 FT DISULFID 51 57
 BY SIMILARITY.

FT DISULFID 52 65 BY SIMILARITY.
 FT MOD_RES 66 66 AMIDATION (G-67 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 69 AA; 7442 MW; E36ECE90BF1B56B0 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 69;
 Best Local Similarity 33.3%; Pred. No. 14;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
 DB 51 CCSPPRCSHPCLC 65

RESULT 5
 KRUB_HUMAN
 ID KRUB_HUMAN STANDARD; PRT; 194 AA.
 AC 075690;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Keratin, ultra high-sulfur matrix protein B (UHS keratin B) (UHS
 DE KerB).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RX MEDLINE-99148005; PubMed-10023043;
 RA Perez C., Autiol J., Gerst C., Bernard B.A., Egly J.-M.;
 RT "Genomic organization and promoter characterization of two human UHS
 RT keratin genes.";
 RL Gene 227:137-148(1999).
 CC -1- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
 CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
 CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
 CC SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
 CC 6-20 KDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
 CC KERATINS (40-56 KDa).
 CC -1- TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
 CC HAIR FOLLICLES.
 CC -1- DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
 CC RICH (SR) REPEATS.
 CC -1- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AJ006692; CA07188.1; -
 DR HSSP: P01053; 1BBI.
 KW Keratin; Repeat; Multigene family.
 SQ SEQUENCE 194 AA; 18094 MW; 8607B2AE906FE44A CRC64;

Query Match 63.6%; Score 35; DB 1; Length 194;
 Best Local Similarity 33.3%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
 DB 46 CCVPACSCSCGSC 60

RESULT 6
 ID CXXA_CONPE STANDARD; PRT; 16 AA.
 AC P50984;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Pn1A.
 OS Conus pennaceus (feathered cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=37335;
 RN [1]
 RP SEQUENCE.

RC TISSUE-Venom;
 RX MEDLINE-94347719; PubMed-8068627;
 RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
 RA Spira M.E., Zlotkin E.;
 RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
 RT acetylcholine receptors.";
 RL Biochemistry 33:9523-9529(1994).
 RN [2]

RP SULFATION OF TYR-15.
 RX MEDLINE-99242956; PubMed-10226369;
 RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
 RA Baldwin M.A., Burlingame A.L.;
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
 RT alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and
 RT phosphopeptides by electrospray, matrix-assisted laser
 RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
 RT spectrometry.";
 RL J. Mass Spectrom. 34:447-454(1999).
 RN [3]

RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 RX MEDLINE-96311277; PubMed-8740364;
 RA Hu S.-H., Gehrmann J., Guedat L.W., Alewood P.F., Craik D.J.,
 RA Martin J.L.;
 RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
 RT antagonist, alpha-conotoxin Pn1A from Conus pennaceus.";
 RL Structure 4:417-423(1996).

CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES. THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
 CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
 CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PDB: 1PEN; 2I-APR-97.

KW postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
 FT DISULFID 2 8
 FT MOD_RES 3 16
 FT MOD_RES 15 15
 FT MOD_RES 16 16
 SQ SEQUENCE 16 AA; 1628 MW; 05310FF9EC99005 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 16;
 Best Local Similarity 33.3%; Pred. No. 8.4;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPCXXXXXXC 17
 DB 2 CCSLPCCANPNPYC 16

RESULT 7
 ID CXXA_CONPE STANDARD; PRT; 16 AA.
 AC P50985;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Pn1B.
 OS Conus pennaceus (feathered cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=37335;

RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=94347719; PubMed=8068627;
 RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
 RA Spira M.E., Zlotkin E.,
 RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
 RT acetylcholine receptors."
 RL Biochemistry 33:9523-9529(1994).
 RN [2]
 RP SUFFATION OF TYR-15
 RX MEDLINE=99242956; PubMed=10226369;
 RA Wolfender J.L., Chu F., Bail H., Wolfender F., Fainzilber M.,
 RA Baldwin M.A., Burlingame A.L.;
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
 RT alpha-Pn1a and alpha-Pn1b: further investigation of labile sulfo- and
 RT phosphopeptides by electrospray, matrix-assisted laser MALDI mass
 RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
 RT spectrometry.";
 RL J. Mass Spectrom. 34:447-454(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 RX MEDLINE=97444322; PubMed=9298951;
 RA Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
 RT "Crystal structure at 1.1-A resolution of alpha-conotoxin Pn1b:
 RT comparison with alpha-conotoxins Pn1a and G1.";
 RL Biochemistry 36:11323-11330(1997).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
 CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
 CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PDB: 1AKG; 20-MAY-98.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 15 15
 FT MOD_RES 16 16
 FT MOD_RES 16 16
 SQ SEQUENCE 16 AA; 1643 MW; 05310FF955D86AFC5 CRC64;
 Query Match 61.8%; Score 34; DB 1; Length 16;
 Best Local Similarity 33.3%; Pred. No. 8.4;
 Matches 5; Conservativity 0; Mismatches 10; Indels 0; Gaps 0;
 QY 3 CCXXPYCXXXXXXC 17
 DB 2 CCSLPALSNPDYC 16
 RESULT 8
 CXAL_CONER STANDARD; PRT; 18 AA.
 ID CXAL_CONER
 AC P50982;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Et.
 OS Conus ermaeus (Atlantic fish-hunting cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conidae; Conidae; Conus.
 OX NCBI_TaxID=55423;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=96062516; PubMed=7578057;
 RA Martinez J.S., Oliviera B.M., Gray W.R., Craig A.G., Groebe D.R.,
 RA Abramson S.N., McIntosh J.M.;
 RT "Alpha-conotoxin Et, a new nicotinic acetylcholine receptor

RT antagonist with novel selectivity.";
 RL Biochemistry 34:14519-14526(1995).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM.
 CC -1- SUBUNIT: Binds nicotinic acetylcholine receptor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; Hydroxylation.
 FT DISULFID 4 10
 FT DISULFID 5 18
 FT MOD_RES 3 3
 FT MOD_RES 18 18
 FT MOD_RES 18 18
 SQ SEQUENCE 18 AA; 2082 MW; 60A61A6C427A6B5E CRC64;
 Query Match 61.8%; Score 34; DB 1; Length 18;
 Best Local Similarity 33.3%; Pred. No. 9;
 Matches 5; Conservativity 0; Mismatches 10; Indels 0; Gaps 0;
 QY 3 CCXXPYCXXXXXXC 17
 DB 4 CCYHPTCNMSNPQIC 18
 RESULT 9
 CXR_CONTU STANDARD; PRT; 19 AA.
 ID CXR_CONTU
 AC P58811;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Rho-conotoxin T1A (Rho-T1A).
 OS Conus tulipa (Fish-hunting cone snail) (Tulip cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conidae; Conidae; Conus.
 OX NCBI_TaxID=6495;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
 RC TISSUE-Venom;
 RX MEDLINE=21419681; PubMed=11528421;
 RA Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
 RA Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
 RA Lewis R.J.;
 RT "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
 RT noradrenaline transporter.";
 RL Nat. Neurosci. 4:902-907(2001).
 CC -1- FUNCTION: Inhibits alpha-1 adrenergic receptors.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=2390.15; METHOD=Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE RHO-CONOTOXIN FAMILY.
 DR PDB: 1IEN; 03-APR-02.
 KW Toxin; Amidation; 3D-structure.
 FT DISULFID 5 11
 FT DISULFID 6 19
 FT MOD_RES 19 19
 FT MOD_RES 19 19
 SQ SEQUENCE 19 AA; 2396 MW; C5917DD62CA89DC CRC64;
 Query Match 61.8%; Score 34; DB 1; Length 19;
 Best Local Similarity 33.3%; Pred. No. 9.3;
 Matches 5; Conservativity 0; Mismatches 10; Indels 0; Gaps 0;
 QY 3 CCXXPYCXXXXXXC 17
 DB 5 CCLIPACRRNHNKFC 19
 RESULT 10
 CXA2_CONTE STANDARD; PRT; 66 AA.
 ID CXA2_CONTE

CC 09XAK7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-type conotoxin Tx2 precursor.
 OS Conus textile (Cloth-of-gold cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6494;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Venom duct;
 RX MEDLINE=20037955; PubMed=10573284;
 RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
 RT "Conopeptides from Conus striatus and Conus textile by CDNA
 cloning";
 RL Peptides 20:1139-1144(1999).
 CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 bind to the nicotinic acetylcholine receptors (nAChR) and thus
 inhibit them (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 FAMILY.

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 DR EMBL: AF146353; A031913.1;
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KM Acetylcholine receptor inhibitor; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 48 POTENTIAL.
 FT PEPTIDE 49 66 ALPHA-TYPE CONOTOXIN TX2.
 FT DISULFID 51 57 BY SIMILARITY.
 FT DISULFID 52 65 BY SIMILARITY.
 SQ SEQUENCE 66 AA: 7234 MW; EDD859BBA94F26F CRC64;
 Query Match 61.8%; Score 34; DB 1; Length 66;
 Best Local Similarity 33.3%; Pred. No. 19;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 3 CCXXPKCXXXXXXC 17
 DB 51 CCSHPACNVDPHEIC 65
 RESULT 11
 ID CXAL_CONEP STANDARD; PRT; 16 AA.
 AC P56638;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Epi.
 OS Conus episcopatus (Bishop's cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=88764;
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 RX MEDLINE=98376423; PubMed=9708977;
 RA Hu S.H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,
 RA Alewood P.F., Lewis R.J., Martin J.L.;
 RT "The 1.1-A resolution crystal structure of [Tyr15]Epi, a novel
 alpha-conotoxin from Conus episcopatus, solved by direct methods";
 RL Biochemistry 37:11425-11433(1998).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY

CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 AND ALPHA-
 CC 3/BETA-4 SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PDB: 1A0W; 13-JAN-99.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KM Acetylcholine receptor inhibitor; Amidation;
 FT SULFATION: 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT DISULFID 15 15
 FT MOD_RES 16 16
 FT MOD_RES 16 16
 SQ SEQUENCE 16 AA: 1792 MW; C6385F376C99B4C CRC64;
 Query Match 60.0%; Score 33; DB 1; Length 16;
 Best Local Similarity 33.3%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 3 CCXXPKCXXXXXXC 17
 DB 2 CCSPPRCNMNNDYC 16
 RESULT 12
 ID MT2_CANGA STANDARD; PRT; 51 AA.
 AC P5114;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metallothionein-II.
 KW MT-II AND MT-IIB.
 OS Candida glabrata (Yeast) (Torulopsis glabrata).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5478;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-38.
 RX MEDLINE=90062075; PubMed=2584191;
 RA Mehra R.K., Garey J.R., Butt T.R., Gray W.R., Winge D.R.;
 RT "Candida glabrata metallothioneins. Cloning and sequence of the genes
 and characterization of proteins";
 RL J. Biol. Chem. 264:19747-19753(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90202916; PubMed=2318858;
 RA Mehra R.K., Garey J.R., Winge D.R.;
 RT "Selective and tandem amplification of a member of the
 metallothionein gene family in Candida glabrata";
 RL J. Biol. Chem. 265:6369-6375(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92267387; PubMed=1339367;
 RA Mehra R.K., Thorvaldsen J.L., Macreadie I.G., Winge D.R.;
 RT "Disruption analysis of metallothionein-encoding genes in Candida
 glabrata";
 RL Gene 114:75-80(1992).
 RN [4]
 RP SEQUENCE OF 1-19 AND 34-51.
 RX MEDLINE=89057829; PubMed=3194392;
 RA Mehra R.K., Tarbet B.E., Gray W.R., Winge D.R.;
 RT "Metal-specific synthesis of two metallothioneins and gamma-glutamyl
 peptides in Candida glabrata";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:8815-8819(1988).
 CC -1- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
 SEQUESTRATION OF TOXIC METAL IONS.
 CC -1- INDUCTION: BOTH MT-I AND MT-II GENES ARE REGULATED BY COPPER ION
 IN A CONCENTRATION-DEPENDENT FASHION, AND BOTH ARE INDUCIBLE BY
 SILVER BUT NOT BY CADMIUM SALTS.

CC -1- MISCELLANEOUS: MT-II MIGHT BIND NEARLY 10 MOL EQ OF CU(II).
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 10.
 CC -----
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 CC -----
 CC EMBL: J05134; AAA35273.1; -
 CC EMBL: J05398; AAA35274.1; -
 CC EMBL: M86727; AAA35275.1; -
 CC PIR: B31252; B31252.
 CC PIR: JCI197; JCI197.
 CC Metal-binding; Metal-thiolate cluster; Copper; Repeat.
 CC FT INIT_MET 0 0
 CC FT REPEAT 42 46
 CC FT REPEAT 47 51
 CC FT VARIANT 1 6 MISSING (IN MT-II).
 CC SQ SEQUENCE 51 AA; 5454 MW; ABD19E511175EF12 CRC64;
 CC
 CC Query Match 60.0%; Score 33; DB 1; Length 51;
 CC Best Local Similarity 57.1%; Pred. No. 23;
 CC Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC QY 3 CCXXPXC 9
 CC ID 1 1 1
 CC Db 23 CCAKPPAC 29
 CC
 CC RESULT 13
 CC MCS_MOUSE
 CC ID MCS_MOUSE STANDARD; PRT; 197 AA.
 CC AC P15265;
 CC DT 01-APR-1990 (Rel. 14, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Sperm mitochondrial capsule selenoprotein (MCS).
 CC GN MCS OR MCS.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Testis;
 CC RX MEDLINE=93039675; PubMed=1418626;
 CC RA Karimpour I., Cutler M., Shih D., Smith J., Kleene K.C.;
 CC RT "Sequence of the gene encoding the mitochondrial capsule
 CC selenoprotein of mouse sperm: identification of three in-phase TGA
 CC selenocysteine codons.";
 CC RL DNA Cell Biol. 11:693-699(1992).
 CC RN [2]
 CC RP SEQUENCE OF 55-197 FROM N.A.
 CC RC TISSUE=Testis;
 CC RX MEDLINE=90152148; PubMed=2301168;
 CC RA Kleene K.C., Smith J., Bozorgzadeh A., Harris M., Hahn L.,
 CC RA Karimpour I., Gerstel J.;
 CC RT "Sequence and developmental expression of the mRNA encoding the
 CC seleno-protein of the sperm mitochondrial capsule in the mouse.";
 CC RL Dev. Biol. 137:395-402(1990).
 CC CC -1- FUNCTION: STRUCTURAL PROTEIN OF THE SPERM MITOCHONDRIAL CAPSULE.
 CC IMPORTANT FOR THE MAINTENANCE AND STABILIZATION OF THE CRESCENT
 CC STRUCTURE OF THE SPERM MITOCHONDRIA.
 CC CC -1- SUBCELLULAR LOCATION: KERATINOUS MITOCHONDRIAL CAPSULE.
 CC CC -1- TISSUE SPECIFICITY: TESTIS.
 CC CC -1- DEVELOPMENTAL STAGE: LATE MEIOTIC AND EARLY HAPLOID CELLS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M88463; AAB08438.1; -
 CC EMBL: M29603; AAA53045.1; -
 CC PIR: A37199; A37199.
 CC MGD: MGI:96945; Mcsp.
 CC Mitochondrion; Selenium; Selenocysteine; Sperm; Testis;
 CC KM Spermatogenesis.
 CC FT SE_CYS 7 7
 CC FT SE_CYS 17 17
 CC FT SE_CYS 34 34
 CC SQ SEQUENCE 197 AA; 21015 MW; 721B84F7129F0281 CRC64;
 CC
 CC Query Match 60.0%; Score 33; DB 1; Length 197;
 CC Best Local Similarity 57.1%; Pred. No. 49;
 CC Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC QY 3 CCXXPXC 9
 CC ID 1 1 1
 CC Db 149 CCAQPTC 155
 CC
 CC RESULT 14
 CC YFH6_YEAST
 CC ID YFH6_YEAST STANDARD; PRT; 535 AA.
 CC AC P43590;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Hypothetical 61.8 kDa peptidase in MPR1-GCN20 intergenic region
 CC DE (EC 3.4.-.-).
 CC GN YFR006W.
 CC OS Saccharomyces cerevisiae (Baker's yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 CC OX NCBI_TaxID=4932;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=5288C / AB972;
 CC RX MEDLINE=95400292; PubMed=7670463;
 CC RA Murkaml Y., Natou M., Hagihara H., Shibata T., Ozawa M.,
 CC RA Sasamura S.-I., Sasamura M., Tsuchiya Y., Soeda E., Yokoyama K.,
 CC RA Yamazaki M., Tashiro H., Eki T.;
 CC RT "Analysis of the nucleotide sequence of chromosome VI from
 CC Saccharomyces cerevisiae.";
 CC RL Nat. Genet. 10:261-268(1995).
 CC CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24B.
 CC -----
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 CC -----
 CC EMBL: D50617; BAA09245.1; -
 CC DR HSPD; P15034; IAI6.
 CC DR MEROPS; M24.UPB; -
 CC DR SGD: S0001902; YFR006W.
 CC DR Interpro: IPR00994; Peptidase M24.
 CC DR Interpro: IPR001131; Xaa-Pro-peptids.
 CC DR Pfam: PF00557; Peptidase_M24; 1.
 CC DR PROSITE: PS00491; PROLINE_PEPTIDASE; 1.
 CC KW Hypothetical protein; Hydrolase; Transmembrane.
 CC FT TRANSMEM 8 24 POTENTIAL.
 CC SQ SEQUENCE 535 AA; 61753 MW; 4D251041CE9627FC CRC64;
 CC
 CC Query Match 60.0%; Score 33; DB 1; Length 535;
 CC Best Local Similarity 57.1%; Pred. No. 86;

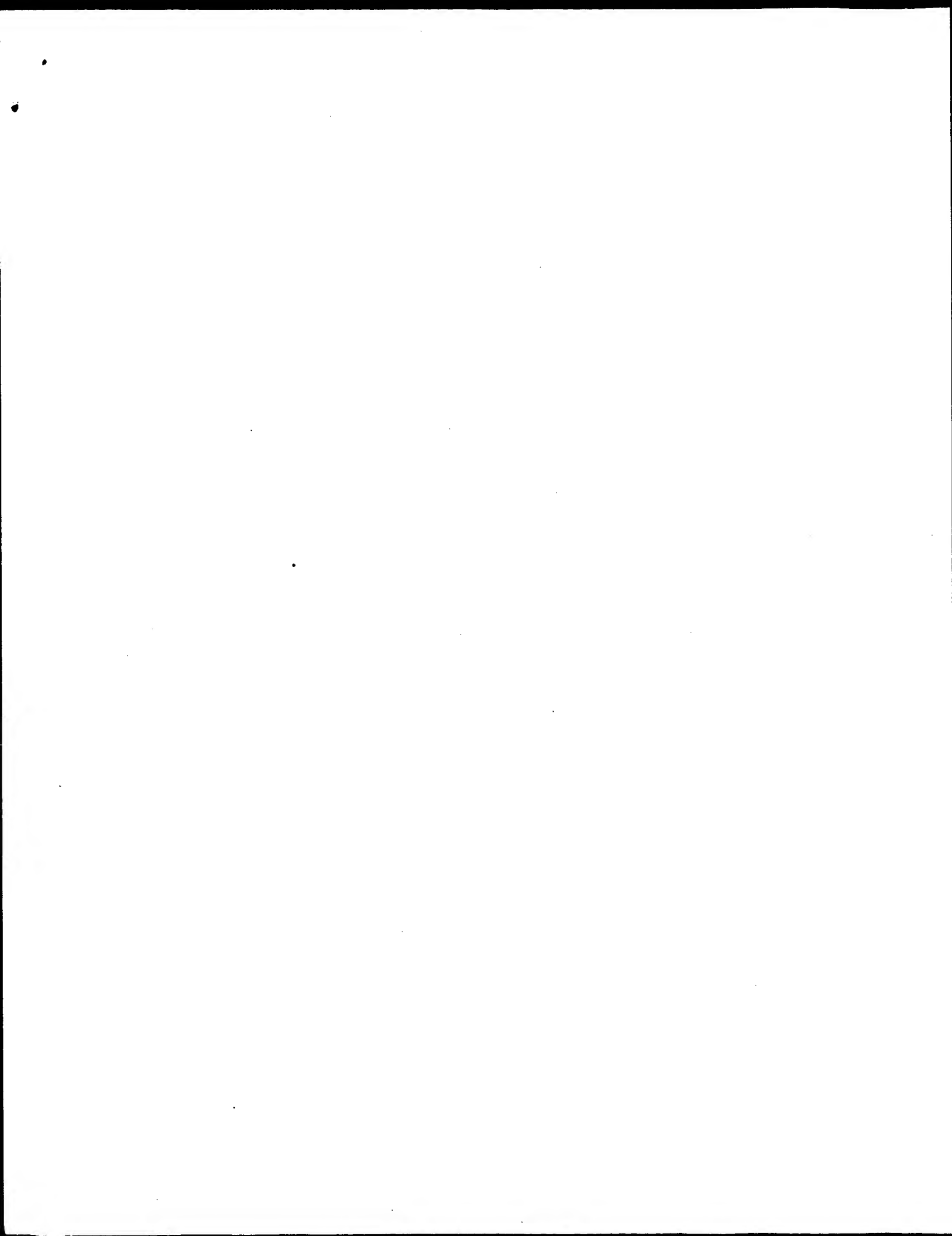
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 CCXXPXC 9
 Db 289 CCSGPC 295

RESULT 15
 ID CXXAL_CONIM STANDARD: PRT: 12 AA.
 AC P50983:
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin IMI.
 OS Conus imperialis (Imperial cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OK NCBI_TaxID=35631;
 RN SEQUENCE, AND SYNTHESIS.
 RP TISSUE-Venom;
 RX MEDLINE=9426689; PubMed=8206995;
 RA McIntosh J.M., Yoshikami D., Mane E., Nielsen D.B., Rivier J.E.,
 RA Gray W.R., Olivera B.M.;
 RT "A nicotinic acetylcholine receptor ligand of unique specificity,
 RT alpha-conotoxin IMI.";
 RL J. Biol. Chem. 269:16733-16739(1994).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=95379776; PubMed=7651351;
 RA Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,
 RA McIntosh J.M.;
 RT "Alpha-conotoxin IMI exhibits subtype-specific nicotinic
 RT acetylcholine receptor blockade: preferential inhibition of homomeric
 RT alpha 7 and alpha 9 receptors.";
 RL Mol. Pharmacol. 48:194-199(1995).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99212205; PubMed=10194298;
 RA Rogers J.P., Lugnbuehl P., Shen G.S., McCabe R.T., Stevens R.C.,
 RA Wenner D.E.;
 RT "NMR solution structure of alpha-conotoxin IMI and comparison to
 RT other conotoxins specific for neuronal nicotinic acetylcholine
 RT receptors.";
 RL Biochemistry 38:3874-3882(1999).
 RN [4]
 RP STRUCTURE BY NMR.
 RX PubMed=10350614;
 RA Gouda H., Hirose S.;
 RT "Solution structure of alpha-conotoxin IMI determined by
 RT two-dimensional NMR spectroscopy.";
 RL Biochim. Biophys. Acta 1431:384-394(1999).
 RN [5]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99158061; PubMed=10050774;
 RA Maslennikov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,
 RA Methfessel C., Tselin V.I., Arseniev A.S.;
 RT "NMR spatial structure of alpha-conotoxin IMI reveals a common
 RT scaffold in small and snake toxins recognizing neuronal nicotinic
 RT acetylcholine receptors.";
 RL FEBS Lett. 444:275-280(1999).
 RN [6]
 RP STRUCTURE BY NMR.
 RX PubMed=10431825;
 RA Lanthanh H., Jegou-Matheron C., Servent D., Menez A., Lancelin J.-M.;
 RT "Minimal conformation of the alpha-conotoxin IMI for the alpha/
 RT neuronal nicotinic acetylcholine receptor recognition: correlated CD,
 RT NMR and binding studies.";
 RL FEBS Lett. 454:293-298(1999).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99324017; PubMed=10395477;

RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;
 RT "Solution structure of alpha-conotoxin IMI by 1H nuclear magnetic
 RT resonance.";
 RL J. Med. Chem. 42:2364-2372(1999).
 RN [8]
 RP MUTAGENESIS OF ASP-5; ARG-7 AND ARG-11, AND STRUCTURE BY NMR OF THESE
 RP THREE MUTANTS.
 RX PubMed=11124036;
 RA Rogers J.P., Lugnbuehl P., Pemberton K., Harty P., Wenner D.E.,
 RA Stevens R.C.;
 RT "Structure-activity relationships in a peptidic alpha7 nicotinic
 RT acetylcholine receptor antagonist.";
 RL J. Mol. Biol. 304:911-926(2000).
 CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
 CC inhibit them. It is highly active against the neuromuscular
 CC receptor in frog but not in mice. In contrast, it induces seizures
 CC when injected centrally in mice and rats. It targets neuronal
 CC nAChRs in mammals. It blocks homomeric alpha-7 nicotinic receptors
 CC with the highest apparent affinity and homomeric alpha-9 receptors
 CC with 8-fold lower affinity. It has no effect on receptors composed
 CC of alpha-2/beta-2, alpha-3/beta-2, alpha-4/beta-2, alpha-2/beta-4,
 CC alpha-3/beta-4, or alpha-4/beta-4 subunit combinations.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PDB: 1IMI; 15-JUN-99.
 DR PDB: 1IMI; 23-APR-99.
 DR PDB: 1CNU; 27-MAY-99.
 DR PDB: 1E74; 27-DEC-00.
 DR PDB: 1E75; 27-DEC-00.
 DR PDB: 1E76; 27-DEC-00.
 DR PDB: 1G2S; 08-NOV-00.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
 FT DISULFID 2 8
 FT MOD.RES 12 12
 FT MUTAGEN 5 5
 FT MUTAGEN 7 7
 FT MUTAGEN 11 11
 SQ SEQUENCE 12 AA; 1357 MW; 9C29CBA545A4176A CRC64;

Query Match 58.2%; Score 32; DB 1; Length 12;
 Best Local Similarity 57.1%; Pred. No. 14;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 CCXXPXC 9
 Db 2 CCSGPC 8

Search completed: January 8, 2003, 15:28:56
 Job time: 8.72727 secs



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OM protein - protein search, using sw model

Run on: January 8, 2003, 15:26:54 ; Search time 25.424 Seconds
(without alignments)
138.766 Million cell updates/sec

Title: US-09-897-465-1

Perfect score: 55

Sequence: 1 XCCXXPCXCCXXXXXC 17

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	61.8	61	5	Q9BP57
2	34	61.8	61	5	Q9BP56
3	34	61.8	189	11	Q9D527
4	34	61.8	560	4	Q9P226
5	33	60.0	113	2	Q9S133
6	33	60.0	152	4	Q9HB04
7	33	60.0	154	2	Q82932
8	33	60.0	169	2	Q9ZGV1
9	33	60.0	181	4	Q9HCR8
10	33	60.0	190	2	Q9AN40
11	33	60.0	196	11	Q9D226
12	33	60.0	197	11	Q70613
13	33	60.0	223	11	Q62220
14	33	60.0	230	11	Q64507
15	33	60.0	255	4	Q9H512
16	33	60.0	275	4	Q9B083

17	33	60.0	363	12	Q69275	Q69275 equine herp
18	33	60.0	406	2	Q93PX0	Q93PX0 shigella so
19	33	60.0	435	10	Q8W2T7	Q8W2T7 oryza sativ
20	33	60.0	542	2	Q59145	Q59145 aeromonas s
21	33	60.0	777	5	Q9VYPI	Q9VYPI drosophila
22	33	60.0	978	5	P91777	P91777 pacifastacu
23	33	60.0	1670	10	Q9LE42	Q9LE42 arabidopsis
24	33	60.0	1978	5	Q9WOM1	Q9WOM1 drosophila
25	33	60.0	3004	5	Q24550	Q24550 drosophila
26	33	60.0	3232	3	Q94205	Q94205 claviceps p
27	33	60.0	4123	4	Q75851	Q75851 homo sapien
28	33	58.2	66	13	Q9PTM2	Q9PTM2 colurnix co
29	33	58.2	113	3	Q08522	Q08522 saccharomyc
30	33	58.2	141	4	Q96AC2	Q96AC2 homo sapien
31	33	58.2	141	11	Q9J796	Q9J796 mus musculu
32	33	58.2	145	11	Q64298	Q64298 ratius norv
33	33	58.2	149	4	Q9NSR8	Q9NSR8 homo sapien
34	33	58.2	154	4	Q9BYO2	Q9BYO2 homo sapien
35	33	58.2	156	11	Q9CTX8	Q9CTX8 mus musculu
36	33	58.2	159	4	Q9BYO3	Q9BYO3 homo sapien
37	33	58.2	159	4	Q9BYO0	Q9BYO0 homo sapien
38	33	58.2	168	11	Q9D732	Q9D732 mus musculu
39	33	58.2	174	4	Q9BYO4	Q9BYO4 homo sapien
40	33	58.2	177	11	Q9D644	Q9D644 mus musculu
41	33	58.2	187	5	Q95PB8	Q95PB8 anopheles g
42	33	58.2	197	5	Q18337	Q18337 caenorhabdi
43	33	58.2	197	6	Q28584	Q28584 ovis aries
44	33	58.2	202	11	Q9CVX6	Q9CVX6 mus musculu
45	33	58.2	210	16	Q9PY90	Q9PY90 xyella fas

ALIGNMENTS

RESULT 1

ID Q9BP57 PRELIMINARY; PRT; 61 AA.
AC Q9BP57;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Conotoxin scaffold 1.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21105969; PubMed-1158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Patinilber M.,
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF215088; AAG60509.1; -.
DR HSSP; P50985; IAKG.
SQ SEQUENCE 61 AA; 6363 MW; 42E003324D66922 CRC64;

Query Match 61.8%; Score 34; DB 5; Length 61;
Best Local Similarity 33.3%; Pred. No. 9.8;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPCXCCXXXXXC 17
DB 46 CCSUPPCALSNPDYC 60

RESULT 2

ID Q9BP56 PRELIMINARY; PRT; 61 AA.
AC Q9BP56;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Conotoxin scafold I.
 OS Conus pennaeus (Feathered cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conidae; Conus.
 OX NCBI_TaxID=37335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21105969; PubMed=11158371;
 RA Conticello S.G., Gildad Y., Avidan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides";
 RL Mol. Biol. Evol. 18:120-131(2001).
 DR EMBL; AF215089; AAG60510.1;...
 DR HSP; P50985; IAKG.
 SQ SEQUENCE 61 AA; 6348 MW; 6FCFD333D306921 CRC64;

Query Match 61.8%; Score 34; DB 5; Length 61;
 Best Local Similarity 33.3%; Pred. No. 9.8;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPCXXXXXXC 17
 Db 46 CCSRPACALSNPDYC 60

RESULT 3

ID 09D527 PRELIMINARY; PRT; 189 AA.

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE 4833428E21RIK protein.

GN 4833428E21RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57Bl/6J; TISSUE=HEAD;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai T., Shunagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleisemann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,

RA Blake J., Boffelli D., Bojunga N., Carinici P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni U., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK014785; BAB29552.1;...
 DR HSSP; P02876; 9WGA.
 DR MGD; MGI:1918873; 4833428E21RIK.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR001305; DnaJ_CXXCXXG.
 DR InterPro; IPR001007; VWF_C.
 DR PROSITE; PS00198; 4FEAS_FERREDOXIN; UNKNOWN_2.
 DR PROSITE; PS00637; DnaJ_CXXCXXG; 1.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_1.
 SQ SEQUENCE 189 AA; 17234 MW; B6A30BF5E2A31E CRC64;

Query Match 61.8%; Score 34; DB 11; Length 189;
 Best Local Similarity 33.3%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPCXXXXXXC 17
 Db 32 CCCVPACSCSCGDC 46

RESULT 4

ID 09P226 PRELIMINARY; PRT; 560 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE KIAA1502 protein (Fragment).

GN KIAA1502.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20277482; PubMed=10819331;

RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.,

RT "Prediction of the coding sequences of unidentified human

RT genes. XVII. The complete sequences of 100 new cDNA clones from brain

RL DNA Res. 7:143-150(2000).

DR EMBL; AB040935; BAA6026.1;...

DR InterPro; IPR002654; GT_25.

DR Pfam; PF01755; Glyco_transf_25; 1.

FT NON_TER 1

FT NON_TER 560

SQ SEQUENCE 560 AA; 63471 MW; 8D41E317E5B74DA CRC64;

Query Match 61.8%; Score 34; DB 4; Length 560;
 Best Local Similarity 33.3%; Pred. No. 27;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPCXXXXXXC 17
 Db 15 CCLQPLCCSTPLHC 29

RESULT 5

ID 09S133 PRELIMINARY; PRT; 113 AA.

AC 09S133;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Orf32 protein.

GN Orf32.

OS Escherichia coli.

OG Plasmid pB171.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9426847; PubMed=10496929;

RA Tohe T., Hayashi T., Han C.G., Schmolnik G.K., Ohsudo E.,

RA Sasaki C.;

RT "Complete DNA sequence and structural analysis of the enteropathogenic

RT Escherichia coli adherence factor plasmid";

RL Infect. Immun. 67:5455-5462(1999).

DR EMBL; AB024946; BAA64867.1;...

KW Plasmid
 SQ SEQUENCE 113 AA; 13016 MW; 1C41D5771CAB475F CRC64;

Query Match 60.0%; Score 33; DB 2; Length 113;

Best Local Similarity 57.1%; Pred. No. 20;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CCXXPXC 9
Db 52 CCSSPDC 58

RESULT 6

ID 09HB04 PRELIMINARY; PRT: 152 AA.
AC 09HB04;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Ras association domain family protein isoform 1G.
GN RASFP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Burbee D.G., Forgacs E., White M.A., Lerman M., Minna J.D.;
RT "RASFP1, a putative Ras effector and tumor suppressor from the human
RT 3p21.3 critical region, contains alternatively spliced messages from
RT two promoters."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF291719; AAG10064.1;
DR InterPro: IPR002219; DAG_PE-bind.
DR Pfam: PF00130; DAG_PE-bind; 1.
DR SMART: SM00109; C1; 1.
DR PROSITE: PSS0081; DAG_PE_BIND_DOM_2; 1.
DR EMBL: AF074613; AAC70083.1;
SQ SEQUENCE 152 AA; 16119 MW; 18403EEC734C2695 CRC64;

Query Match 60.0%; Score 33; DB 4; Length 152;
Best Local Similarity 57.1%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CCXXPXC 9
Db 139 CCQAPAC 145

RESULT 7

ID 082932 PRELIMINARY; PRT: 154 AA.
AC 082932;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Transposase.
GN ISB1.
OS Escherichia coli O157:H7.
OC Plasmid pO157.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7;
RA MEDLINE=98290540; PubMed=9628576;
RA Makino K., Ishii K., Yasunaga T., Hattori M., Yokoyama K.,
RA Yutsudo H.C., Kubota Y., Yamachi Y., Iida T., Yamamoto K., Honda T.,
RA Han C.G., Ohtsubo E., Kasamatsu M., Hayashi T., Kuhara S.,
RA Shinagawa H.;
RT "Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an
RT enterohemorrhagic Escherichia coli O157:H7 derived from Sakai
RT outbreak."
RL DNA Res. 5:1-9(1998).
DR EMBL: AB011549; BA031831.1;
KW Plasmid.
SQ SEQUENCE 154 AA; 17879 MW; AD87A5690D208279 CRC64;

Query Match 60.0%; Score 33; DB 2; Length 154;
Best Local Similarity 57.1%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CCXXPXC 9
Db 52 CCSSPDC 58

RESULT 8

ID 09ZGV1 PRELIMINARY; PRT: 169 AA.
AC 09ZGV1;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE Transposase.
GN I7015.
OS Escherichia coli O157:H7.
OC Plasmid pO157.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EDL933;
RX MEDLINE=98391744; PubMed=9722640;
RA Burdall V., Shao Y., Perna N.T., Plunkett G., Sofia H.J.,
RA Blattner F.R.;
RT "The complete DNA sequence and analysis of the large virulence plasmid
RT of Escherichia coli O157:H7."
RL Nucleic Acids Res. 26:4196-4204(1998).
DR EMBL: AF074613; AAC70083.1;
KW Plasmid.
SQ SEQUENCE 169 AA; 19444 MW; 61BA8D4E57EE02E CRC64;

Query Match 60.0%; Score 33; DB 2; Length 169;
Best Local Similarity 57.1%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CCXXPXC 9
Db 67 CCSSPDC 73

RESULT 9

ID 09HCR8 PRELIMINARY; PRT: 181 AA.
AC 09HCR8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE OGCI type 1e (Fragment).
GN OGCI type 1E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20184065; PubMed=10717238;
RA Shimura K., Kohno T., Takeuchi-Sasaki M., Maeda M., Segawa T.,
RA Kamo T., Sugimura H., Yokota J.;
RT "Expression of the OGCI-type 1a (nuclear form) protein in cancerous
RT and non-cancerous human cells."
RL Int. J. Oncol. 16:701-707(2000).
DR EMBL: AB037879; BAB13294.1;
DR InterPro: IPR003265; Endo_3c.
DR Pfam: PF00730; HNH-GPD; 1.
KW NON_TER
SQ SEQUENCE 181 AA; 19492 MW; 3634F234D8BD3457 CRC64;

Query Match 60.0%; Score 33; DB 4; Length 181;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCXXPXC 9
DB 94 CCXVPTC 100

RESULT 10

ID 09A040 PRELIMINARY; PRT; 190 AA.
AC 09A040;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE ID582.
GN ID582.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-110SPC4;
RX MEDLINE-21101824; PubMed-1157954;
RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
Hennecke H.;
RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
DNA region of the Bradyrhizobium japonicum chromosome.";
RL J. Bacteriol. 183:1405-1412(2001).
DR EMBL: AF322013; AAC60938.1; -
SQ SEQUENCE 190 AA; 21308 MW; 78624D3CFC62DB5F CRC64;

Query Match 60.0%; Score 33; DB 2; Length 190;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCXXPXC 9
DB 37 CCXSPAC 43

RESULT 11

ID 09D226 PRELIMINARY; PRT; 196 AA.
AC 09D226;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE A030007E19RIK protein.
GN A030007E19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-SKIN;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
Schrml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmking L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).
DR EMBL: AK020699; BAB32180.1; -
DR HSSP: P10969; 1WGT.
DR MGD: MGI:1924465; A030007E19RIK.
DR InterPro: IPR001450; 4Fe4S_ferredoxin.
DR InterPro: IPR001305; DnaL_CXXCXXG.
DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_3.
DR PROSITE: PS00637; DNaL_CXXCXXG; 3.
SQ SEQUENCE 196 AA; 17777 MW; 2136738FD496D815 CRC64;

Query Match 60.0%; Score 33; DB 11; Length 196;
Best Local Similarity 33.3%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCXXPXCXXXXXC 17
DB 19 CCXVPTCSCSCGCC 33

RESULT 12

ID 070613 PRELIMINARY; PRT; 197 AA.
AC 070613;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1999 (TREMblrel. 11, last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, last annotation update)
DE Mitochondrial capsule selenoprotein.
GN MSCP OR MCS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93039675; PubMed-1418626;
RA Karimpour I., Cutler M., Shin D., Smith J., Kleene K.C.;
RT "Sequence of the gene encoding the mitochondrial capsule selenoprotein
of mouse sperm: identification of three in-phase TGA selenocysteine
RT codons.";
RL DNA Cell Biol. 11:693-699(1992).
DR EMBL: S49657; AAC08282.1; -
DR EMBL: S49654; AAC08282.1; JOINED.
DR EMBL: S49659; AAC08283.1; -
DR MGD: MGI:96945; MSCP.
DR InterPro: IPR003267; Pro_rich.
DR InterPro: IPR002965; P_rich_extensn.
DR InterPro: IPR001007; VWF_C.
DR PRINTS: PR01217; PRICHEXTENSN.
DR PRINTS: PR00021; PRORIC.
DR PROSITE: PS01208; VWF_C; UNKNOWN_1.
SQ SEQUENCE 197 AA; 21036 MW; 03B657A0F769D5B0 CRC64;

Query Match 60.0%; Score 33; DB 11; Length 197;
Best Local Similarity 57.1%; Pred. No. 26;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCXXPXC 9
DB 149 CCAQPTC 155

RESULT 13

ID 062220 PRELIMINARY; PRT; 223 AA.
AC 062220;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)

DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Serine 2 ultra high sulfur protein.
 GN KRTAP5-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE=91065960; PubMed=2250030;
 RA Wood L., Mills M., Hatzembuhler N., Vogeli G.;
 RT "Serine-rich ultra high sulfur protein gene expression in murine hair
 RT and skin during the hair cycle."
 RL J. Biol. Chem. 265:21375-21380(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE=91154184; PubMed=1840598;
 RA Wood L., Mills M., Hatzembuhler N., Vogeli G.;
 RT "Additions and Corrections: Serine-rich ultra high sulfur protein gene
 RT expression in murine hair and skin during the hair cycle."
 RL J. Biol. Chem. 266:4024-4024(1991).
 DR EMBL; M37760; AAA40107.1; -;
 DR HSSP; P01064; 1P12.
 DR MGD; MGI:1354758; Krtap5-4.
 DR InterPro: IPR001450; 4Fe4S-ferredoxin.
 DR InterPro: IPR001007; VWF_C.
 DR PROSITE; PS00198; 4FE4S-FERREDOXIN; UNKNOWN_2.
 DR PROSITE; PS01208; VWF; UNKNOWN_1.
 SQ SEQUENCE 223 AA; 21442 MW; C654BDB9FD08C59A CRC64;

Query Match
 Best Local Similarity 60.0%; Score 33; DB 11; Length 223;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPXCXXXXXXC 17
 Db 26 CCVPCVSCSSCGGC 40

RESULT 14
 ID 064507 PRELIMINARY; PRT; 230 AA.
 AC 064507;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Serine 1 ultra high sulfur protein.
 GN KRTAP5-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE=91065960; PubMed=2250030;
 RA Wood L., Mills M., Hatzembuhler N., Vogeli G.;
 RT "Serine-rich ultra high sulfur protein gene expression in murine hair
 RT and skin during the hair cycle."
 RL J. Biol. Chem. 265:21375-21380(1990).
 DR EMBL; M37759; AAA40106.1; -;
 DR HSSP; P01064; 1P12.
 DR MGD; MGI:1354732; Krtap5-1.
 DR InterPro: IPR001450; 4Fe4S-ferredoxin.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001305; DnaI_CXXCXGXG.
 DR InterPro: IPR001007; VWF_C.
 DR PROSITE; PS00198; 4FE4S-FERREDOXIN; UNKNOWN_1.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00637; DnaI_CXXCXGXG; UNKNOWN_1.
 DR PROSITE; PS01208; VWF; UNKNOWN_3.

SQ SEQUENCE 230 AA; 21781 MW; 6CC50B41B2137C23 CRC64;
 Query Match
 Best Local Similarity 60.0%; Score 33; DB 11; Length 230;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPXCXXXXXXC 17
 Db 53 CCVPCVSCSSCGGC 67

RESULT 15
 ID 09H5H2 PRELIMINARY; PRT; 255 AA.
 AC 09H5H2;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE CDNA: FLJ23439 fis, clone HS100184.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SMALL INTESTINE;
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohnori Y., Ota T., Suzuki Y.,
 RA Isogai T., Sugano S.;
 RT "MDO human cDNA sequencing project."
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AK027092; BAB15654.1; -;
 DR InterPro: IPR000305; UvrC_N.
 DR SMART; SM00465; GYFC; 1.
 SQ SEQUENCE 255 AA; 28175 MW; CCDC5C958B8C51BB CRC64;

Query Match
 Best Local Similarity 60.0%; Score 33; DB 4; Length 255;
 Matches 5; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCXXPXCXXXXXXC 17
 Db 201 CCFHPCGLRAHYIC 215

Search completed: January 8, 2003, 15:29:54
 Job time : 27.2424 secs

